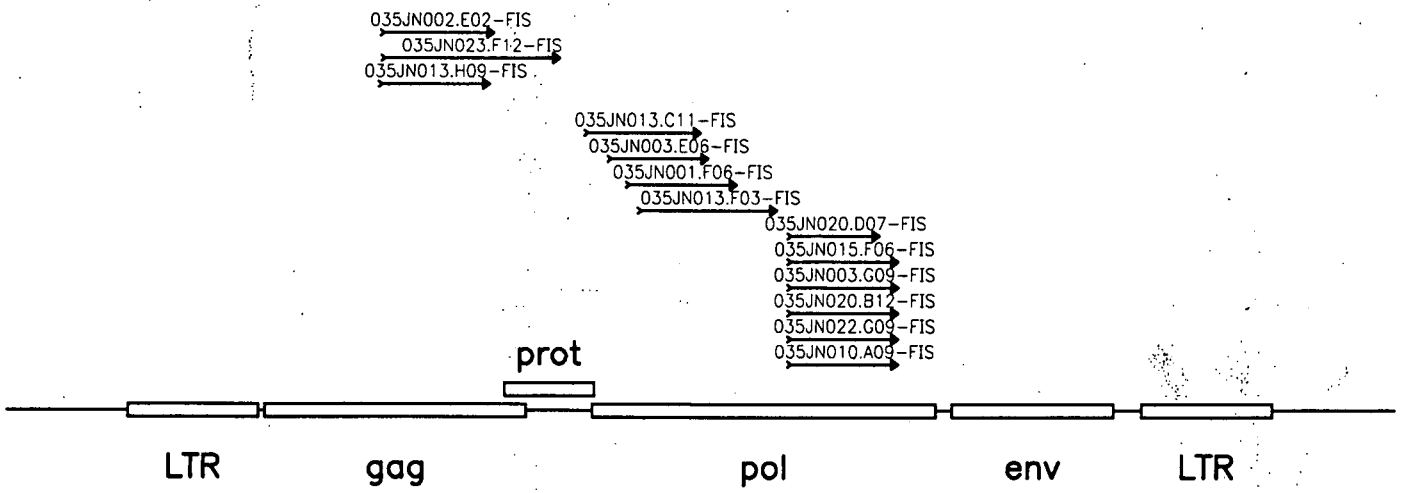

FIG. 1

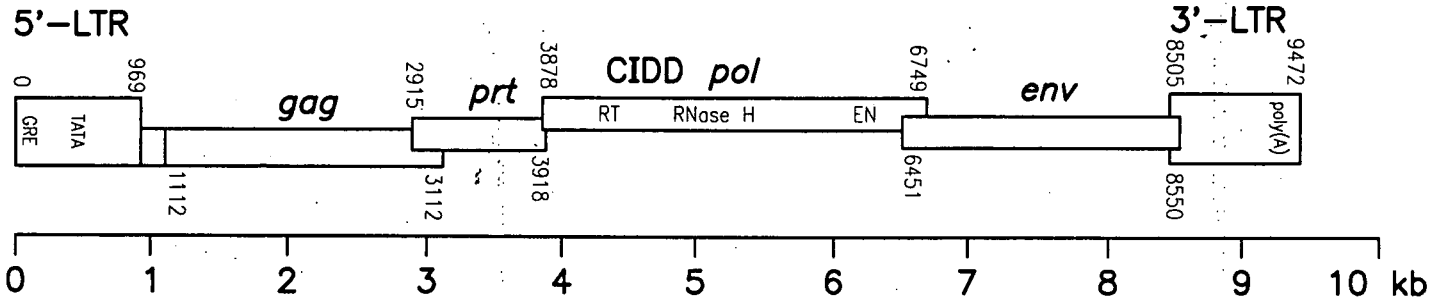

FIG. 2

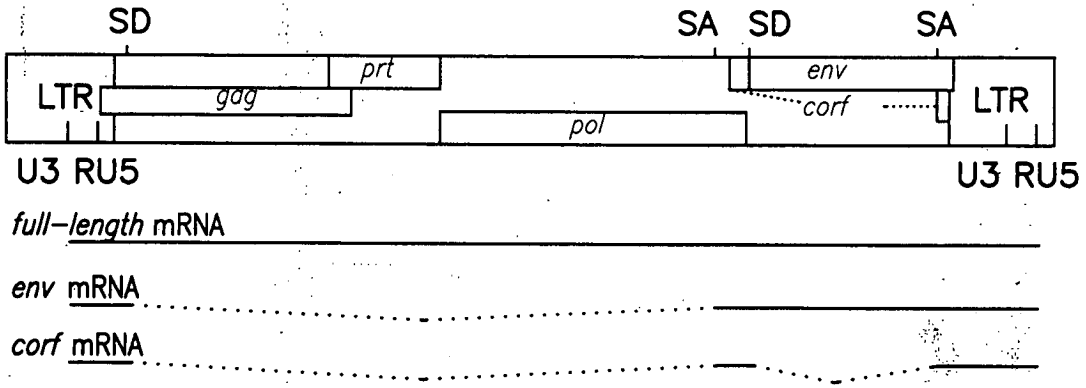
SD
SA
SD
SA
LTR
gag
prt
pol
env
corf
LTR
U3 RU5
U3 RU5
full-length mRNA
env mRNA
corf mRNA

FIG. 3

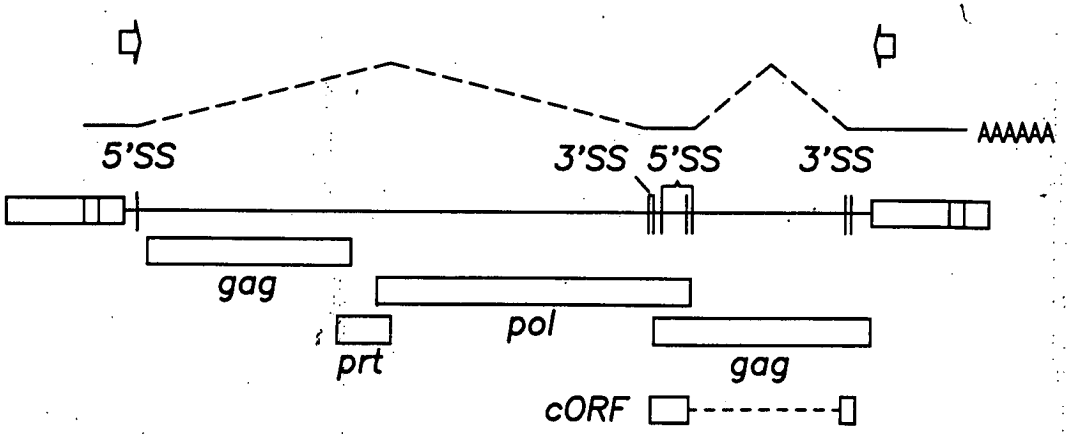
AAAAAA
5'SS
3'SS
5'SS
3'SS
gag
pol
prt
gag
cORF

FIG. 4

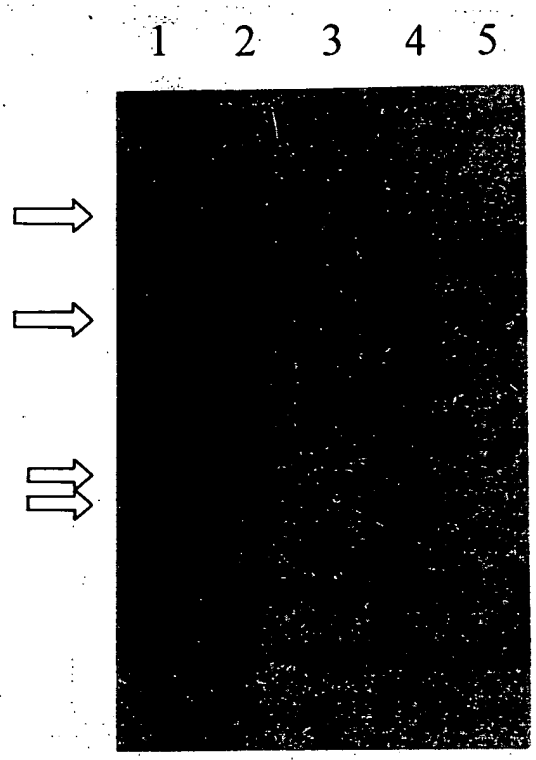

FIG. 5

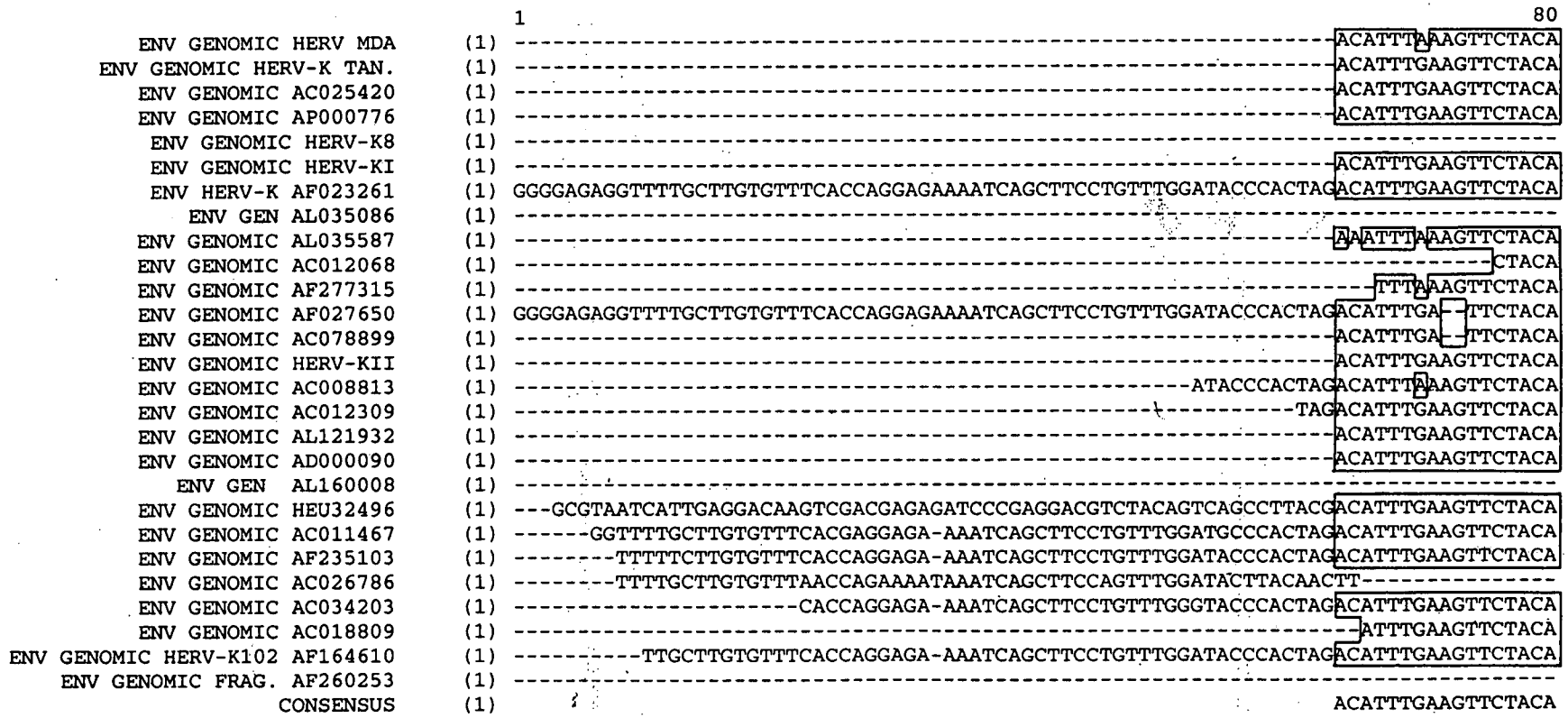
1
80
ENV GENOMIC HERV MDA (1) ----------ACATTTGAAGTTCTACA
ENV GENOMIC HERV-K TAN. (1) ----------ACATTTGAAGTTCTACA
ENV GENOMIC AC025420 (1) ----------ACATTTGAAGTTCTACA
ENV GENOMIC AP000776 (1) ----------ACATTTGAAGTTCTACA
ENV GENOMIC HERV-K8 (1) ----------
ENV GENOMIC HERV-KI (1) ----------ACATTTGAAGTTCTACA
ENV HERV-K AF023261 (1) GGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGAAAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGAAGTTCTACA
ENV GEN AL035086 (1) ----------
ENV GENOMIC AL035587 (1) ----------AAATTTGAAGTTCTACA
ENV GENOMIC AC012068 (1) ----------CTACA
ENV GENOMIC AF277315 (1) ----------TTTGAAGTTCTACA
ENV GENOMIC AF027650 (1) GGGGAGAGGTTTTGCTTGTGTTTCACCAGGAGAAAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGA--TTCTACA
ENV GENOMIC AC078899 (1) ----------ACATTTGA--TTCTACA
ENV GENOMIC HERV-KII (1) ----------ACATTTGAAGTTCTACA
ENV GENOMIC AC008813 (1) ----------ATACCCACTAGACATTTGAAGTTCTACA
ENV GENOMIC AC012309 (1) ----------TAGACATTTGAAGTTCTACA
ENV GENOMIC AL121932 (1) ----------ACATTTGAAGTTCTACA
ENV GENOMIC AD000090 (1) ----------ACATTTGAAGTTCTACA
ENV GEN AL160008 (1) ----------
ENV GENOMIC HEU32496 (1) ---GCGTAATCATTGAGGACAAGTCGACGAGAGATCCCGAGGACGTCTACAGTCAGCCTTACGACATTTGAAGTTCTACA
ENV GENOMIC AC011467 (1) ------GGTTTTGCTTGTGTTTCACGAGGAGA-AAATCAGCTTCCTGTTTGGATGCCCACTAGACATTTGAAGTTCTACA
ENV GENOMIC AF235103 (1) --------TTTTTCTTGTGTTTCACCAGGAGA-AAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGAAGTTCTACA
ENV GENOMIC AC026786 (1) --------TTTTGCTTGTGTTTAACCAGAAAATAAATCAGCTTCCAGTTTGGATACTTACAACTT----------
ENV GENOMIC AC034203 (1) ----------CACCAGGAGA-AAATCAGCTTCCTGTTTGGGTACCCACTAGACATTTGAAGTTCTACA
ENV GENOMIC AC018809 (1) ----------ATTTGAAGTTCTACA
ENV GENOMIC HERV-K102 AF164610 (1) ----------TTGCTTGTGTTTCACCAGGAGA-AAATCAGCTTCCTGTTTGGATACCCACTAGACATTTGAAGTTCTACA
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (1) ACATTTGAAGTTCTACA

FIG. 6-1

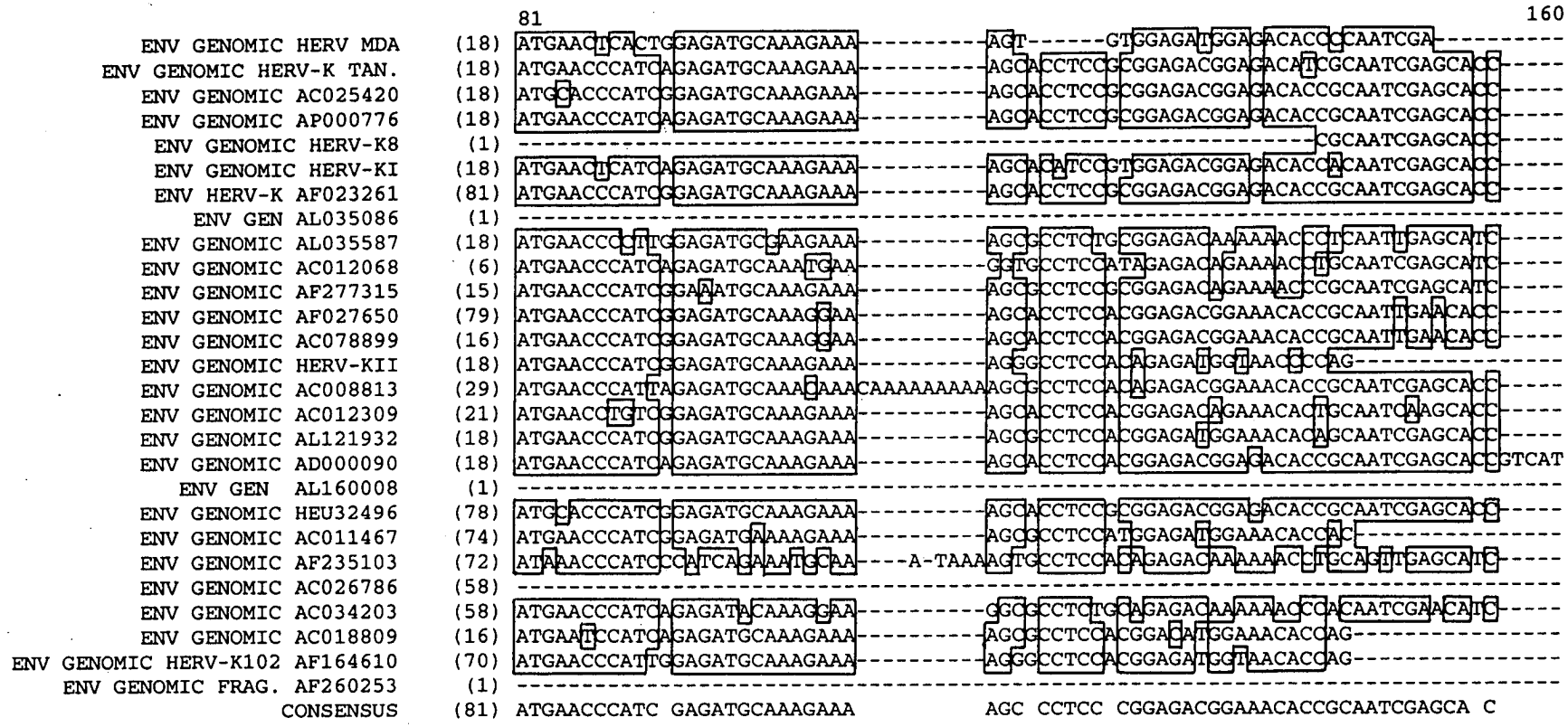
81
160
ENV GENOMIC HERV MDA (18) ATGAACTCACTGGAGATGCAAAGAAA---------AGT------GTGGAGATGGAGACACCGCAATCGA----------
ENV GENOMIC HERV-K TAN. (18) ATGAACCCATCAGAGATGCAAAGAAA---------AGCACCTCCGCGGAGACGGAGACATCGCAATCGAGCACC-----
ENV GENOMIC AC025420 (18) ATGCACCCATCGGAGATGCAAAGAAA---------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
ENV GENOMIC AP000776 (18) ATGAACCCATCAGAGATGCAAAGAAA---------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
ENV GENOMIC HERV-K8 (1) ----------CGCAATCGAGCACC-----
ENV GENOMIC HERV-KI (18) ATGAACTCATCAGAGATGCAAAGAAA---------AGCACATCCGTGGAGACGGAGACACCACAATCGAGCACC-----
ENV HERV-K AF023261 (81) ATGAACCCATCGGAGATGCAAAGAAA---------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
ENV GEN AL035086 (1) ----------
ENV GENOMIC AL035587 (18) ATGAACCCGTTCGGAGATGCGAAGAAA---------AGCGCCTCTGCGGAGACAAAAAACCGTCAATTGAGCATC-----
ENV GENOMIC AC012068 (6) ATGAACCCATCAGAGATGCAAATGAA---------GGTGCCTCCATAGAGACAGAAAACCTGCAATCGAGCATC-----
ENV GENOMIC AF277315 (15) ATGAACCCATCGGAAATGCAAAGAAA---------AGCGCCTCCGCGGAGACAGAAAACCCGCAATCGAGCATC-----
ENV GENOMIC AF027650 (79) ATGAACCCATCGGAGATGCAAAGGAA---------AGCACCTCCACGGAGACGGAAACACCGCAATTGAACACC-----
ENV GENOMIC AC078899 (16) ATGAACCCATCGGAGATGCAAAGGAA---------AGCACCTCCACGGAGACGGAAACACCGCAATTGAACACC-----
ENV GENOMIC HERV-KII (18) ATGAACCCATCGGAGATGCAAAGAAA---------AGGGCCTCCACAGAGATTGGTAACCCCAG----------
ENV GENOMIC AC008813 (29) ATGAACCCATTAGAGATGCAAACAAACAAAAAAAAAAGCGCCTCCACAGAGACGGAAACACCGCAATCGAGCACC-----
ENV GENOMIC AC012309 (21) ATGAACCTGTCGGAGATGCAAAGAAA---------AGCACCTCCACGGAGACAGAAACACTGCAATCAAGCACC-----
ENV GENOMIC AL121932 (18) ATGAACCCATCGGAGATGCAAAGAAA---------AGCGCCTCCACGGAGATTGGAAACACAGCAATCGAGCACC-----
ENV GENOMIC AD000090 (18) ATGAACCCATCAGAGATGCAAAGAAA---------AGCACCTCCACGGAGACGGAGACACCGCAATCGAGCACCGTCAT
ENV GEN AL160008 (1) ----------
ENV GENOMIC HEU32496 (78) ATGCACCCATCGGAGATGCAAAGAAA---------AGCACCTCCGCGGAGACGGAGACACCGCAATCGAGCACC-----
ENV GENOMIC AC011467 (74) ATGAACCCATCGGAGATGAAAAGAAA---------AGCGCCTCCATGGAGATGGAAACACCAC----------
ENV GENOMIC AF235103 (72) ATAAACCCATCCCATCAGAAATGCAA----A-TAAAAGTGCCTCCACAGAGACAAAAAACCTGCAGTTGAGCATC-----
ENV GENOMIC AC026786 (58) ----------
ENV GENOMIC AC034203 (58) ATGAACCCATCAGAGATACAAAGGAA---------GGCGCCTCTGCAGAGACAAAAAACCCACAATCGAACATC-----
ENV GENOMIC AC018809 (16) ATGAATCCATCAGAGATGCAAAGAAA---------AGCGCCTCCACGGACATGGAAACACCAG----------
ENV GENOMIC HERV-K102 AF164610 (70) ATGAACCCATTGGAGATGCAAAGAAA---------AGGGCCTCCACGGAGATGGTAACACCAG----------
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (81) ATGAACCCATC GAGATGCAAAGAAA AGC CCTCC CGGAGACGGAAACACCGCAATCGAGCA C

FIG. 6-2

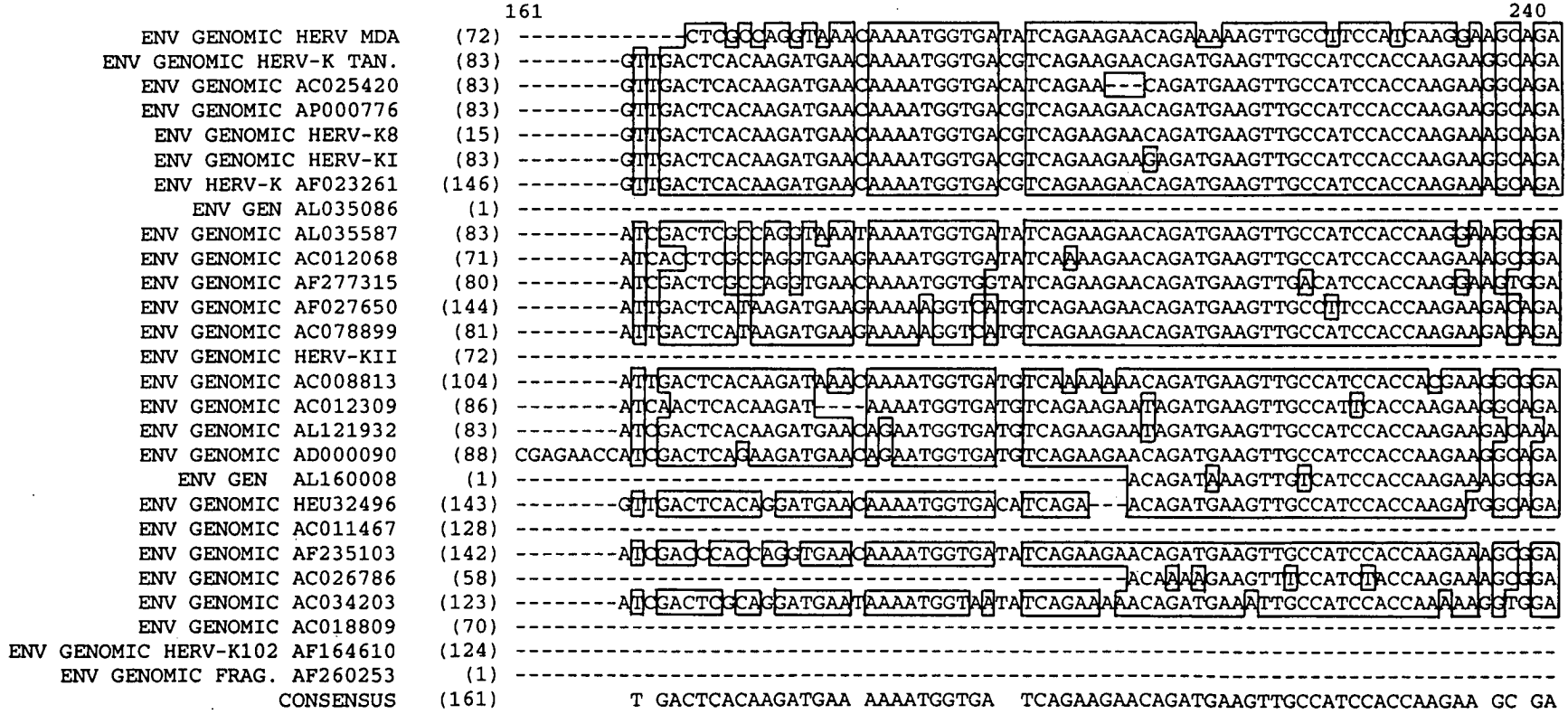
161
240
ENV GENOMIC HERV MDA (72)
ENV GENOMIC HERV-K TAN. (83)
ENV GENOMIC AC025420 (83)
ENV GENOMIC AP000776 (83)
ENV GENOMIC HERV-K8 (15)
ENV GENOMIC HERV-KI (83)
ENV HERV-K AF023261 (146)
ENV GEN AL035086 (1)
ENV GENOMIC AL035587 (83)
ENV GENOMIC AC012068 (71)
ENV GENOMIC AF277315 (80)
ENV GENOMIC AF027650 (144)
ENV GENOMIC AC078899 (81)
ENV GENOMIC HERV-KII (72)
ENV GENOMIC AC008813 (104)
ENV GENOMIC AC012309 (86)
ENV GENOMIC AL121932 (83)
ENV GENOMIC AD000090 (88)
ENV GEN AL160008 (1)
ENV GENOMIC HEU32496 (143)
ENV GENOMIC AC011467 (128)
ENV GENOMIC AF235103 (142)
ENV GENOMIC AC026786 (58)
ENV GENOMIC AC034203 (123)
ENV GENOMIC AC018809 (70)
ENV GENOMIC HERV-K102 AF164610 (124)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (161)
T GACTCACAAGATGAA AAAATGGTGA TCAGAAGAACAGATGAAGTTGCCATCCACCAAGAA GC GA

FIG. 6-3

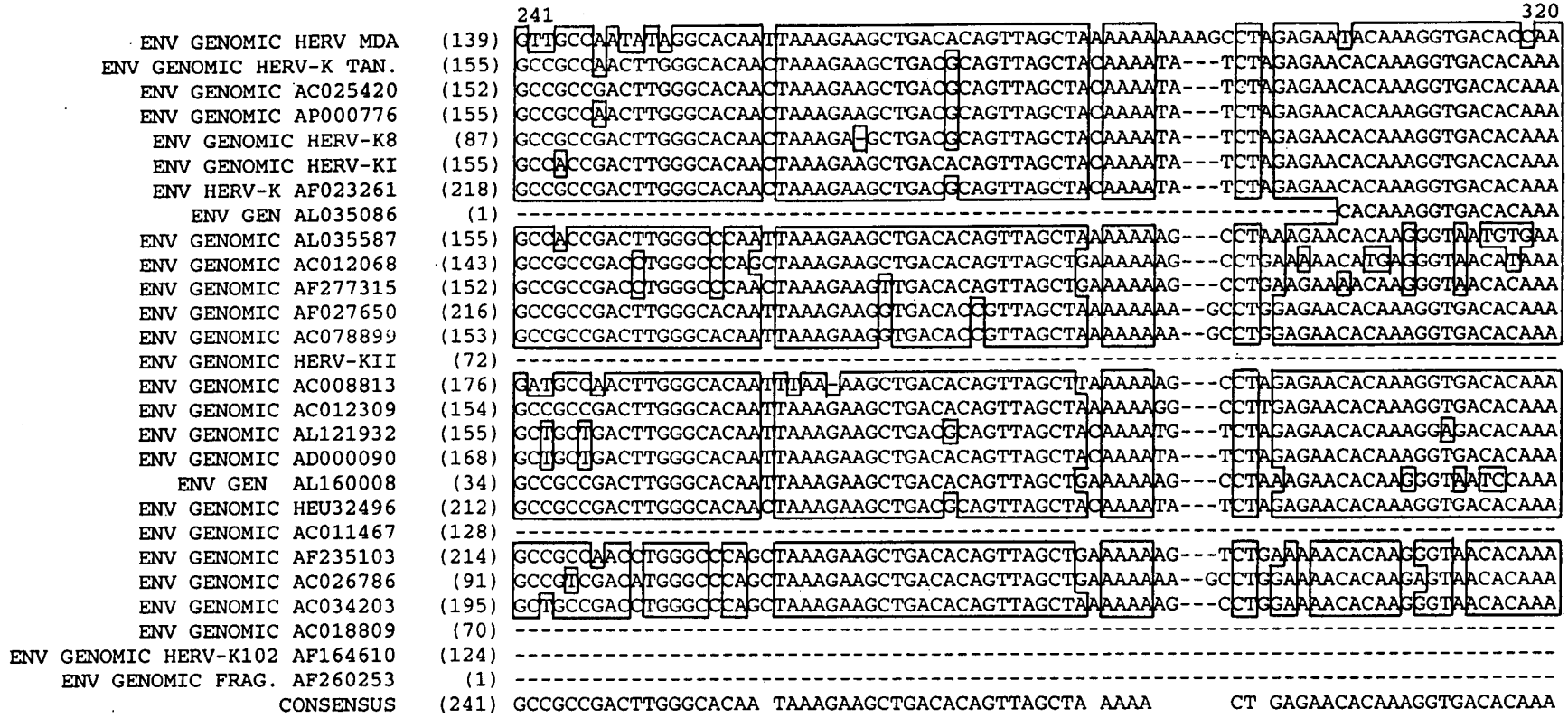
241
320
ENV GENOMIC HERV MDA (139)
ENV GENOMIC HERV-K TAN. (155)
ENV GENOMIC AC025420 (152)
ENV GENOMIC AP000776 (155)
ENV GENOMIC HERV-K8 (87)
ENV GENOMIC HERV-KI (155)
ENV HERV-K AF023261 (218)
ENV GEN AL035086 (1)
ENV GENOMIC AL035587 (155)
ENV GENOMIC AC012068 (143)
ENV GENOMIC AF277315 (152)
ENV GENOMIC AF027650 (216)
ENV GENOMIC AC078899 (153)
ENV GENOMIC HERV-KII (72)
ENV GENOMIC AC008813 (176)
ENV GENOMIC AC012309 (154)
ENV GENOMIC AL121932 (155)
ENV GENOMIC AD000090 (168)
ENV GEN AL160008 (34)
ENV GENOMIC HEU32496 (212)
ENV GENOMIC AC011467 (128)
ENV GENOMIC AF235103 (214)
ENV GENOMIC AC026786 (91)
ENV GENOMIC AC034203 (195)
ENV GENOMIC AC018809 (70)
ENV GENOMIC HERV-K102 AF164610 (124)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (241) GCCGCCGACTTGGGCACAA TAAAGAAGCTGACACAGTTAGCTA AAAA CT GAGAACACAAAGGTGACACAAA

FIG. 6-4

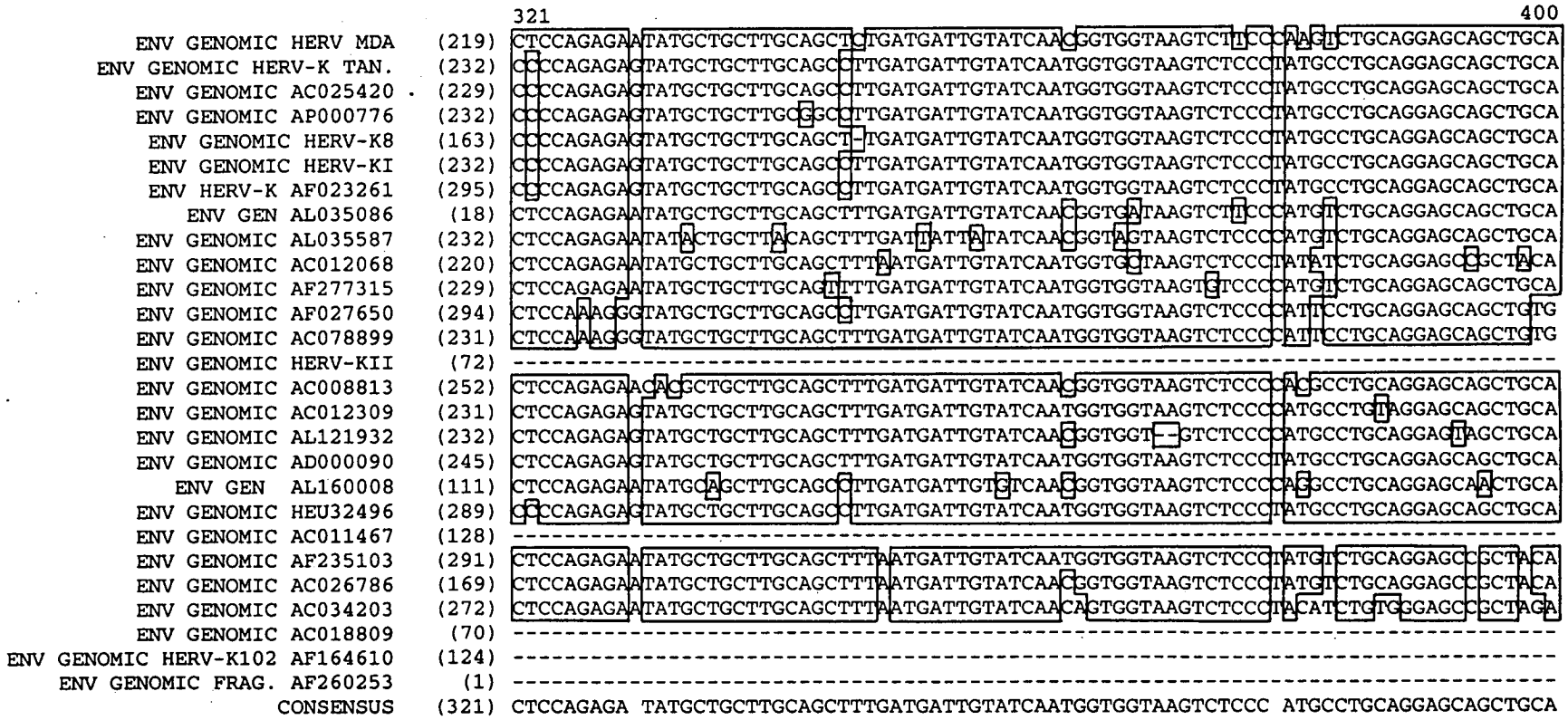
321
400
ENV GENOMIC HERV MDA (219) CTCCAGAGAATATGCTGCTTGCAGCTCTGATGATTGTATCAACGGTGGTAAGTCTTTCCCAAGTCTGCAGGAGCAGCTGCA
ENV GENOMIC HERV-K TAN. (232) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GENOMIC AC025420 (229) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GENOMIC AP000776 (232) CCCCAGAGAGTATGCTGCTTGCGGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GENOMIC HERV-K8 (163) CCCCAGAGAGTATGCTGCTTGCAGCT-TGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GENOMIC HERV-KI (232) CCCCAGAGAGTATGCTGCTTGCAGCCTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV HERV-K AF023261 (295) CGCCAGAGAGTATGCTGCTTGCAGCGTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GEN AL035086 (18) CTCCAGAGAATATGCTGCTTGCAGCTTTGATGATTGTATCAACGGTGATAAGTCTTTCCCATGTCTGCAGGAGCAGCTGCA
ENV GENOMIC AL035587 (232) CTCCAGAGAATATACTGCTTACAGCTTTGATTATTATATCAACGGTAGTAAGTCTCCCCATGTCTGCAGGAGCAGCTGCA
ENV GENOMIC AC012068 (220) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAATGGTGGTAAGTCTCCCTATATCTGCAGGAGCGGCTACA
ENV GENOMIC AF277315 (229) CTCCAGAGAATATGCTGCTTGCAGTTTTGATGATTGTATCAATGGTGGTAAGTGTCCCCATGTCTGCAGGAGCAGCTGCA
ENV GENOMIC AF027650 (294) CTCCAAAGGGTATGCTGCTTGCAGCGTTGATGATTGTATCAATGGTGGTAAGTCTCCCCATTCCTGCAGGAGCAGCTGTG
ENV GENOMIC AC078899 (231) CTCCAAAGGGTATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCCCATTCCTGCAGGAGCAGCTGTG
ENV GENOMIC HERV-KII (72) ----------
ENV GENOMIC AC008813 (252) CTCCAGAGAAGAGGCTGCTTGCAGCTTTGATGATTGTATCAAGGTGGTGGTAAGTCTCCCCAGGCCTGCAGGAGCAGCTGCA
ENV GENOMIC AC012309 (231) CTCCAGAGAGTATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCCCATGCCTGTAGGAGCAGCTGCA
ENV GENOMIC AL121932 (232) CTCCAGAGAGTATGCTGCTTGCAGCTTTGATGATTGTATCAAGGGTGGTC-GTCTCCCCATGCCTGCAGGAGTAGCTGCA
ENV GENOMIC AD000090 (245) CTCCAGAGAGTATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GEN AL160008 (111) CTCCAGAGAATATGCAGCTTGCAGCGTTGATGATTGTGTCAAGGGTGGTAAGTCTCCCCAGGCCTGCAGGAGCAACTGCA
ENV GENOMIC HEU32496 (289) GTCCAGAGAGTATGCTGCTTGCAGCGTTGATGATTGTATCAATGGTGGTAAGTCTCCCTATGCCTGCAGGAGCAGCTGCA
ENV GENOMIC AC011467 (128) ----------
ENV GENOMIC AF235103 (291) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAATGGTGGTAAGTCTCCCTATGTCTGCAGGAGCCGCTACA
ENV GENOMIC AC026786 (169) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAACGGTGGTAAGTCTCCCTATGTCTGCAGGAGCCGCTACA
ENV GENOMIC AC034203 (272) CTCCAGAGAATATGCTGCTTGCAGCTTTAATGATTGTATCAACAGTGGTAAGTCTCCCTACATCTGTGGGAGCCGCTAGA
ENV GENOMIC AC018809 (70) ----------
ENV GENOMIC HERV-K102 AF164610 (124) ----------
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (321) CTCCAGAGA TATGCTGCTTGCAGCTTTGATGATTGTATCAATGGTGGTAAGTCTCCC ATGCCTGCAGGAGCAGCTGCA

FIG. 6-5

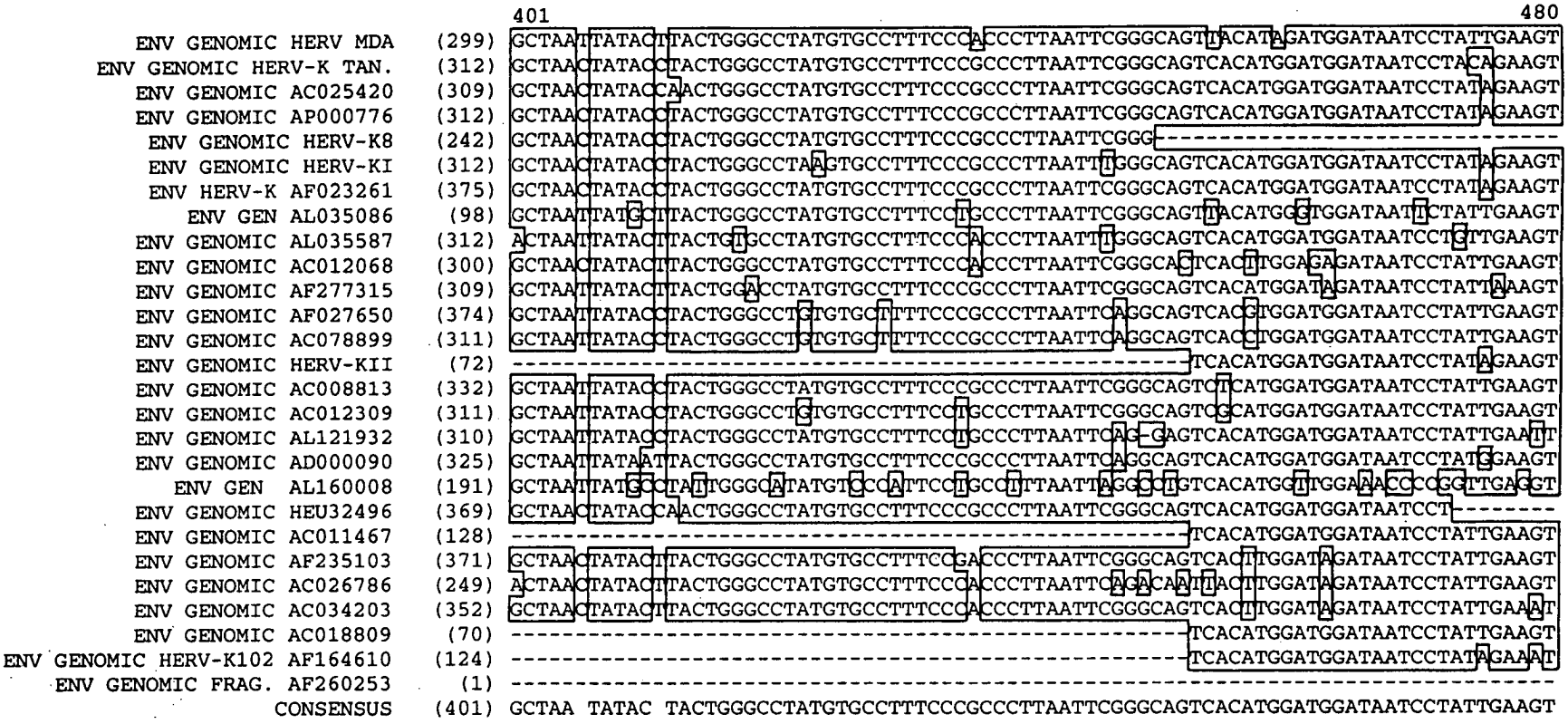
401
480
ENV GENOMIC HERV MDA (299) GCTAATTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCGGGCAGTTACATAGATGGATAATCCTATTGAAGT
ENV GENOMIC HERV-K TAN. (312) GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTACAGAAGT
ENV GENOMIC AC025420 (309) GCTAACTATACCAACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATAGAAGT
ENV GENOMIC AP000776 (312) GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATAGAAGT
ENV GENOMIC HERV-K8 (242) GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGG----------
ENV GENOMIC HERV-KI (312) GCTAACTATACCTACTGGGCCTAAGTGCCTTTCCCGCCCTTAATTTGGGCAGTCACATGGATGGATAATCCTATAGAAGT
ENV HERV-K AF023261 (375) GCTAACTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATAGAAGT
ENV GEN AL035086 (98) GCTAATTATGCTTACTGGGCCTATGTGCCTTTCCTGCCCTTAATTCGGGCAGTTACATGGGTGGATAATTCTATTGAAGT
ENV GENOMIC AL035587 (312) ACTAATTATACTTACTGTGCCTATGTGCCTTTCCCACCCTTAATTTGGGCAGTCACATGGATGGATAATCCTGTTGAAGT
ENV GENOMIC AC012068 (300) GCTAACTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCGGGCAGTCACTTGGAGAGATAATCCTATTGAAGT
ENV GENOMIC AF277315 (309) GCTAATTATACTTACTGGACCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATAGATAATCCTATTAAAGT
ENV GENOMIC AF027650 (374) GCTAATTATACCTACTGGGCCTGTGTGCTTTTCCCGCCCTTAATTCAGGCAGTCACGTGGATGGATAATCCTATTGAAGT
ENV GENOMIC AC078899 (311) GCTAATTATACCTACTGGGCCTGTGTGCTTTTCCCGCCCTTAATTCAGGCAGTCACCTGGATGGATAATCCTATTGAAGT
ENV GENOMIC HERV-KII (72) ----------TCACATGGATGGATAATCCTATAGAAGT
ENV GENOMIC AC008813 (332) GCTAATTATACCTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCTCATGGATGGATAATCCTATTGAAGT
ENV GENOMIC AC012309 (311) GCTAATTATACCTACTGGGCCTGTGTGCCTTTCCTGCCCTTAATTCGGGCAGTCGCATGGATGGATAATCCTATTGAAGT
ENV GENOMIC AL121932 (310) GCTAATTATACCTACTGGGCCTATGTGCCTTTCCTGCCCTTAATTCAG-GAGTCACATGGATGGATAATCCTATTGAATT
ENV GENOMIC AD000090 (325) GCTAATTATAATTACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCAGGCAGTCACATGGATGGATAATCCTATTGAAGT
ENV GEN AL160008 (191) GCTAATTATGCCTATTGGGCATATGTGCCATTCCTGCCTTTAATTAGGCGTGTCACATGGTTGGAAACCCCGGTTGAGGT
ENV GENOMIC HEU32496 (369) GCTAACTATACCAACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCT---------
ENV GENOMIC AC011467 (128) ----------TCACATGGATGGATAATCCTATTGAAGT
ENV GENOMIC AF235103 (371) GCTAACTATACTTACTGGGCCTATGTGCCTTTCCGACCCTTAATTCGGGCAGTCACTTGGATAGATAATCCTATTGAAGT
ENV GENOMIC AC026786 (249) ACTAACTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCAGGCAGTTACTTGGATAGATAATCCTATTGAAGT
ENV GENOMIC AC034203 (352) GCTAACTATACTTACTGGGCCTATGTGCCTTTCCCACCCTTAATTCGGGCAGTCACTTGGATAGATAATCCTATTGAAAT
ENV GENOMIC AC018809 (70) ----------TCACATGGATGGATAATCCTATTGAAGT
ENV GENOMIC HERV-K102 AF164610 (124) ----------TCACATGGATGGATAATCCTATTAGAAAT
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (401) GCTAA TATAC TACTGGGCCTATGTGCCTTTCCCGCCCTTAATTCGGGCAGTCACATGGATGGATAATCCTATTGAAGT

FIG. 6-6

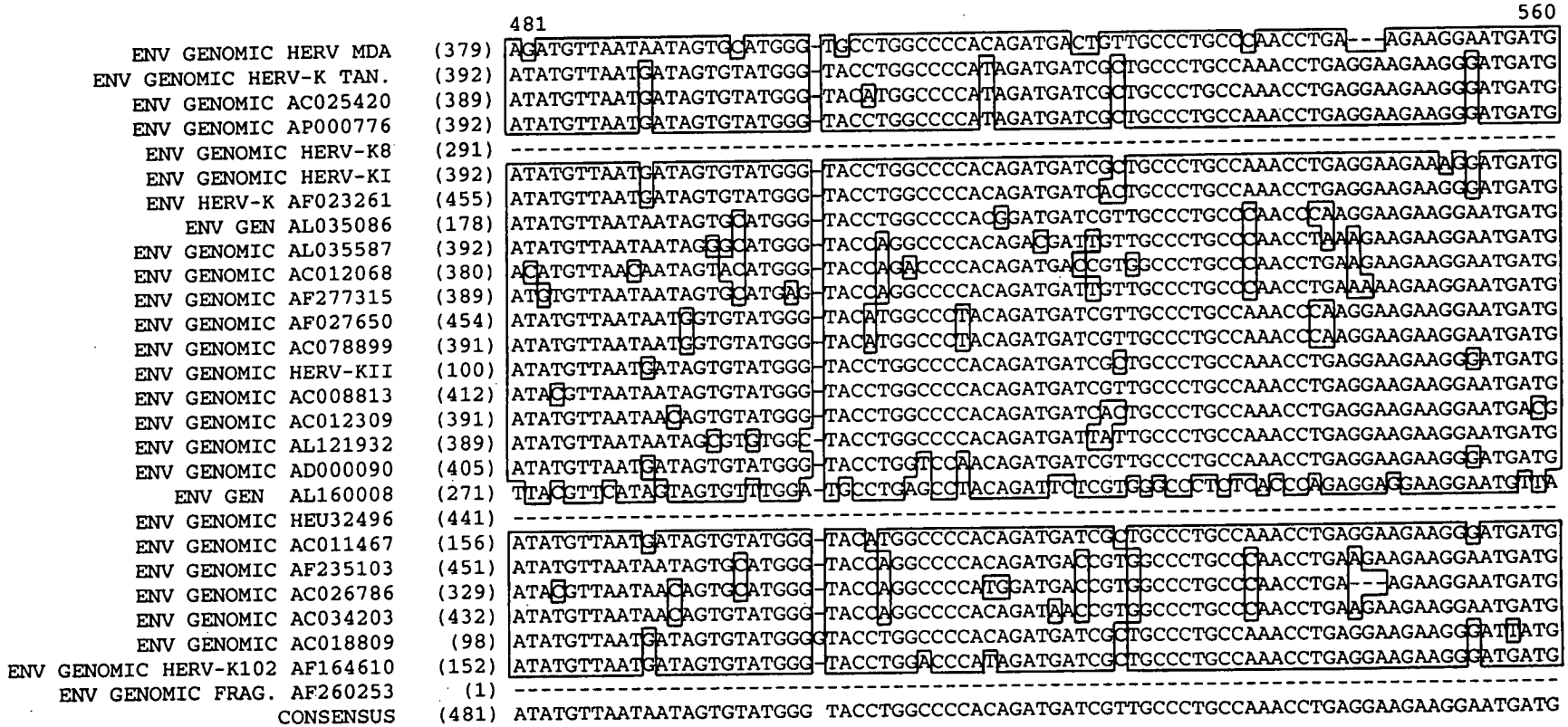
481
560
ENV GENOMIC HERV MDA (379)
ENV GENOMIC HERV-K TAN. (392)
ENV GENOMIC AC025420 (389)
ENV GENOMIC AP000776 (392)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (392)
ENV HERV-K AF023261 (455)
ENV GEN AL035086 (178)
ENV GENOMIC AL035587 (392)
ENV GENOMIC AC012068 (380)
ENV GENOMIC AF277315 (389)
ENV GENOMIC AF027650 (454)
ENV GENOMIC AC078899 (391)
ENV GENOMIC HERV-KII (100)
ENV GENOMIC AC008813 (412)
ENV GENOMIC AC012309 (391)
ENV GENOMIC AL121932 (389)
ENV GENOMIC AD000090 (405)
ENV GEN AL160008 (271)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (156)
ENV GENOMIC AF235103 (451)
ENV GENOMIC AC026786 (329)
ENV GENOMIC AC034203 (432)
ENV GENOMIC AC018809 (98)
ENV GENOMIC HERV-K102 AF164610 (152)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (481) ATATGTTAATAATAGTGTATGGG TACCTGGCCCCACAGATGATCGTTGCCCTGCCAAACCTGAGGAAGAAGGAATGATG

FIG. 6-7

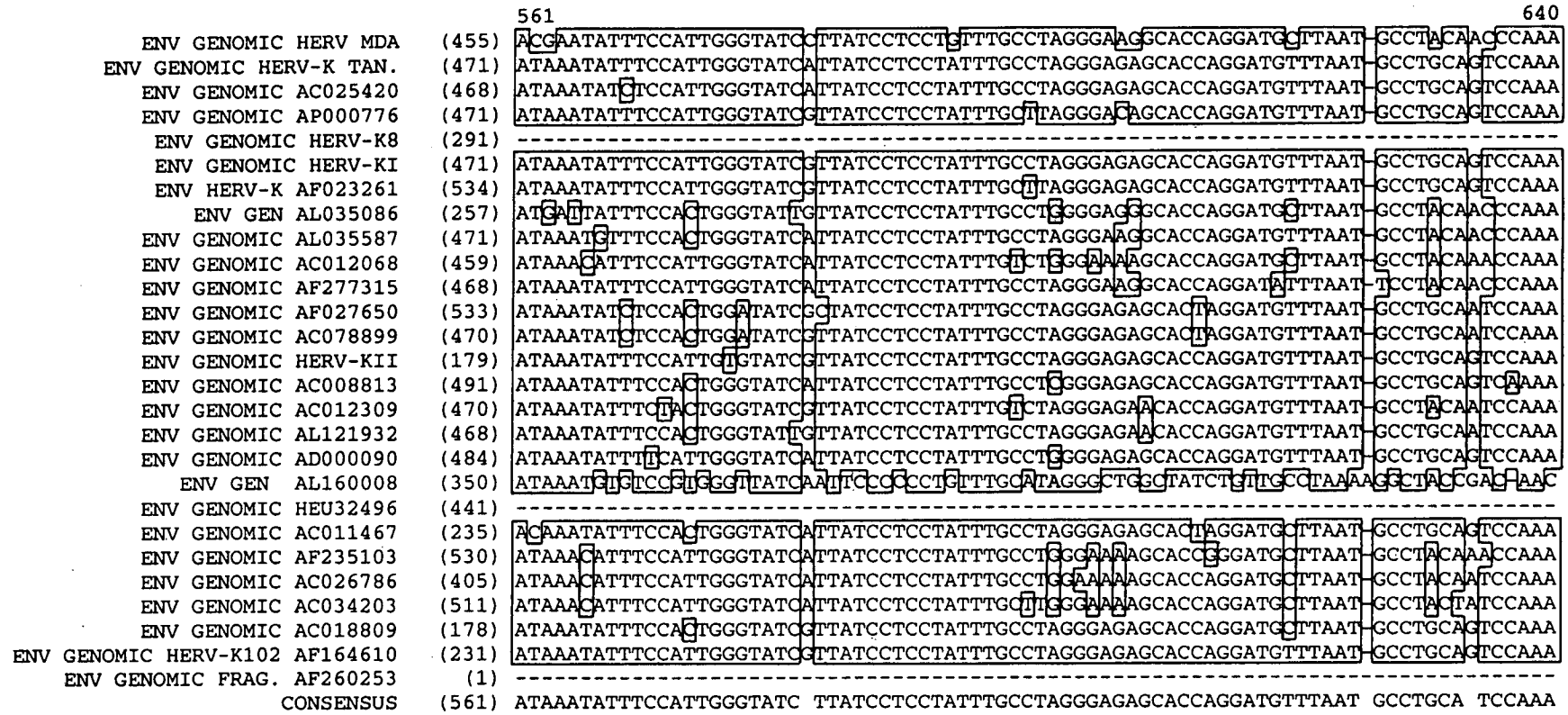
561
640
ENV GENOMIC HERV MDA (455)
ENV GENOMIC HERV-K TAN. (471)
ENV GENOMIC AC025420 (468)
ENV GENOMIC AP000776 (471)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (471)
ENV HERV-K AF023261 (534)
ENV GEN AL035086 (257)
ENV GENOMIC AL035587 (471)
ENV GENOMIC AC012068 (459)
ENV GENOMIC AF277315 (468)
ENV GENOMIC AF027650 (533)
ENV GENOMIC AC078899 (470)
ENV GENOMIC HERV-KII (179)
ENV GENOMIC AC008813 (491)
ENV GENOMIC AC012309 (470)
ENV GENOMIC AL121932 (468)
ENV GENOMIC AD000090 (484)
ENV GEN AL160008 (350)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (235)
ENV GENOMIC AF235103 (530)
ENV GENOMIC AC026786 (405)
ENV GENOMIC AC034203 (511)
ENV GENOMIC AC018809 (178)
ENV GENOMIC HERV-K102 AF164610 (231)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (561) ATAAATATTTCCATTGGGTATC TTATCCTCCTATTTGCCTAGGGAGAGCACCAGGATGTTTAAT GCCTGCA TCCAAA

FIG. 6-8

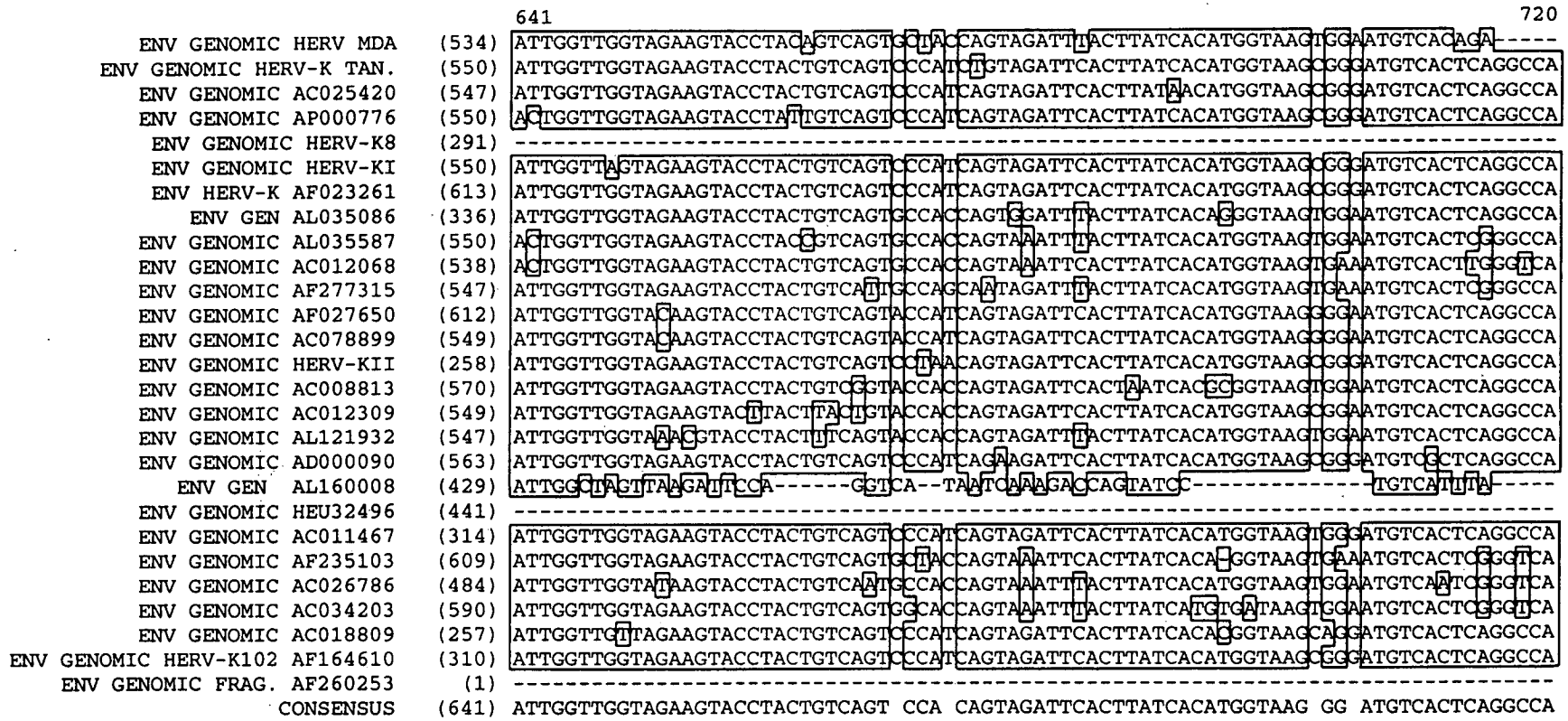
641
720
ENV GENOMIC HERV MDA (534)
ENV GENOMIC HERV-K TAN. (550)
ENV GENOMIC AC025420 (547)
ENV GENOMIC AP000776 (550)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (550)
ENV HERV-K AF023261 (613)
ENV GEN AL035086 (336)
ENV GENOMIC AL035587 (550)
ENV GENOMIC AC012068 (538)
ENV GENOMIC AF277315 (547)
ENV GENOMIC AF027650 (612)
ENV GENOMIC AC078899 (549)
ENV GENOMIC HERV-KII (258)
ENV GENOMIC AC008813 (570)
ENV GENOMIC AC012309 (549)
ENV GENOMIC AL121932 (547)
ENV GENOMIC AD000090 (563)
ENV GEN AL160008 (429)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (314)
ENV GENOMIC AF235103 (609)
ENV GENOMIC AC026786 (484)
ENV GENOMIC AC034203 (590)
ENV GENOMIC AC018809 (257)
ENV GENOMIC HERV-K102 AF164610 (310)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (641) ATTGGTTGGTAGAAGTACCTACTGTCAGT CCA CAGTAGATTCACTTATCACATGGTAAG GG ATGTCACTCAGGCCA

FIG. 6-9

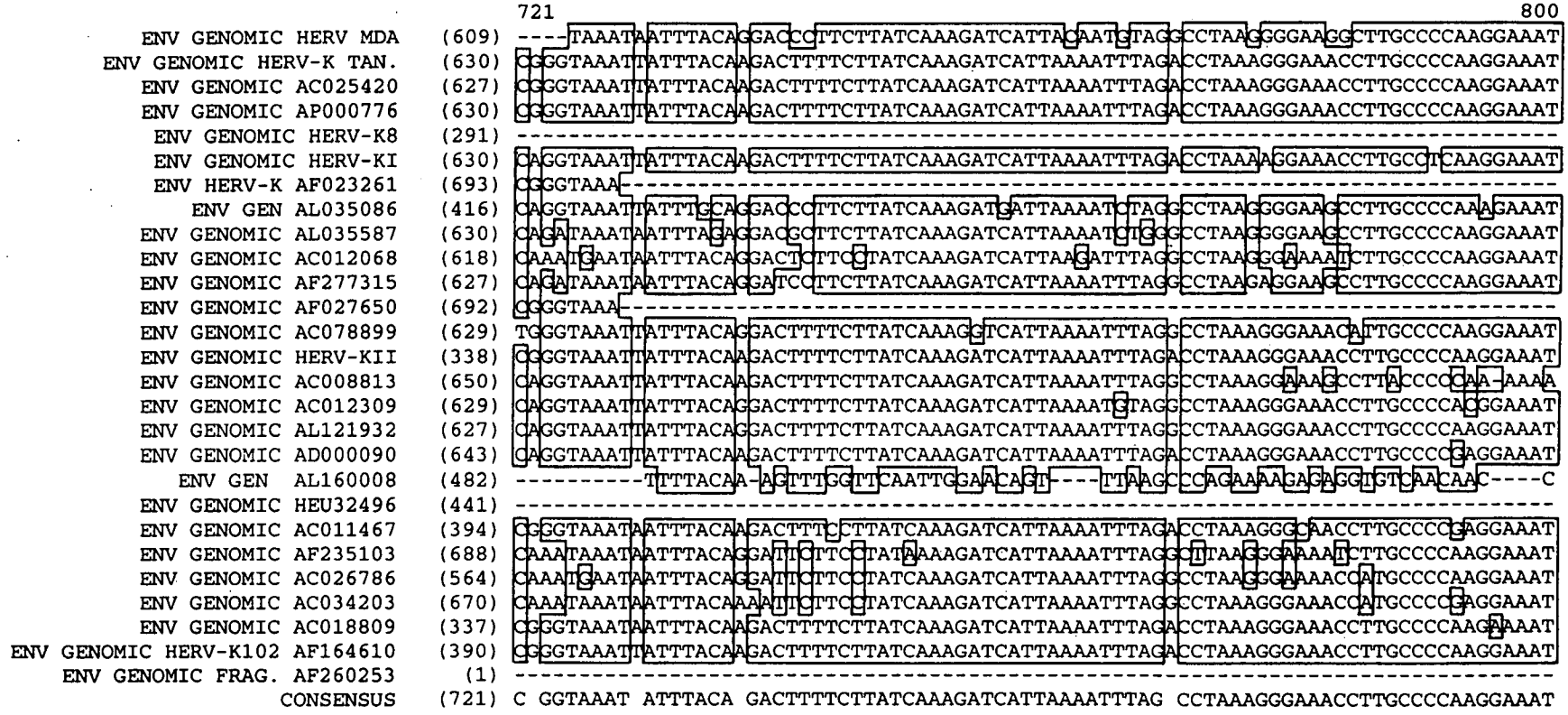
721
800
ENV GENOMIC HERV MDA (609)
ENV GENOMIC HERV-K TAN. (630)
ENV GENOMIC AC025420 (627)
ENV GENOMIC AP000776 (630)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (630)
ENV HERV-K AF023261 (693)
ENV GEN AL035086 (416)
ENV GENOMIC AL035587 (630)
ENV GENOMIC AC012068 (618)
ENV GENOMIC AF277315 (627)
ENV GENOMIC AF027650 (692)
ENV GENOMIC AC078899 (629)
ENV GENOMIC HERV-KII (338)
ENV GENOMIC AC008813 (650)
ENV GENOMIC AC012309 (629)
ENV GENOMIC AL121932 (627)
ENV GENOMIC AD000090 (643)
ENV GEN AL160008 (482)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (394)
ENV GENOMIC AF235103 (688)
ENV GENOMIC AC026786 (564)
ENV GENOMIC AC034203 (670)
ENV GENOMIC AC018809 (337)
ENV GENOMIC HERV-K102 AF164610 (390)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (721) C GGTAAAT ATTTACA GACTTTTCTTATCAAAGATCATTAAAATTTAG CCTAAAGGGAAACCTTGCCCCAAGGAAAT

FIG. 6-10

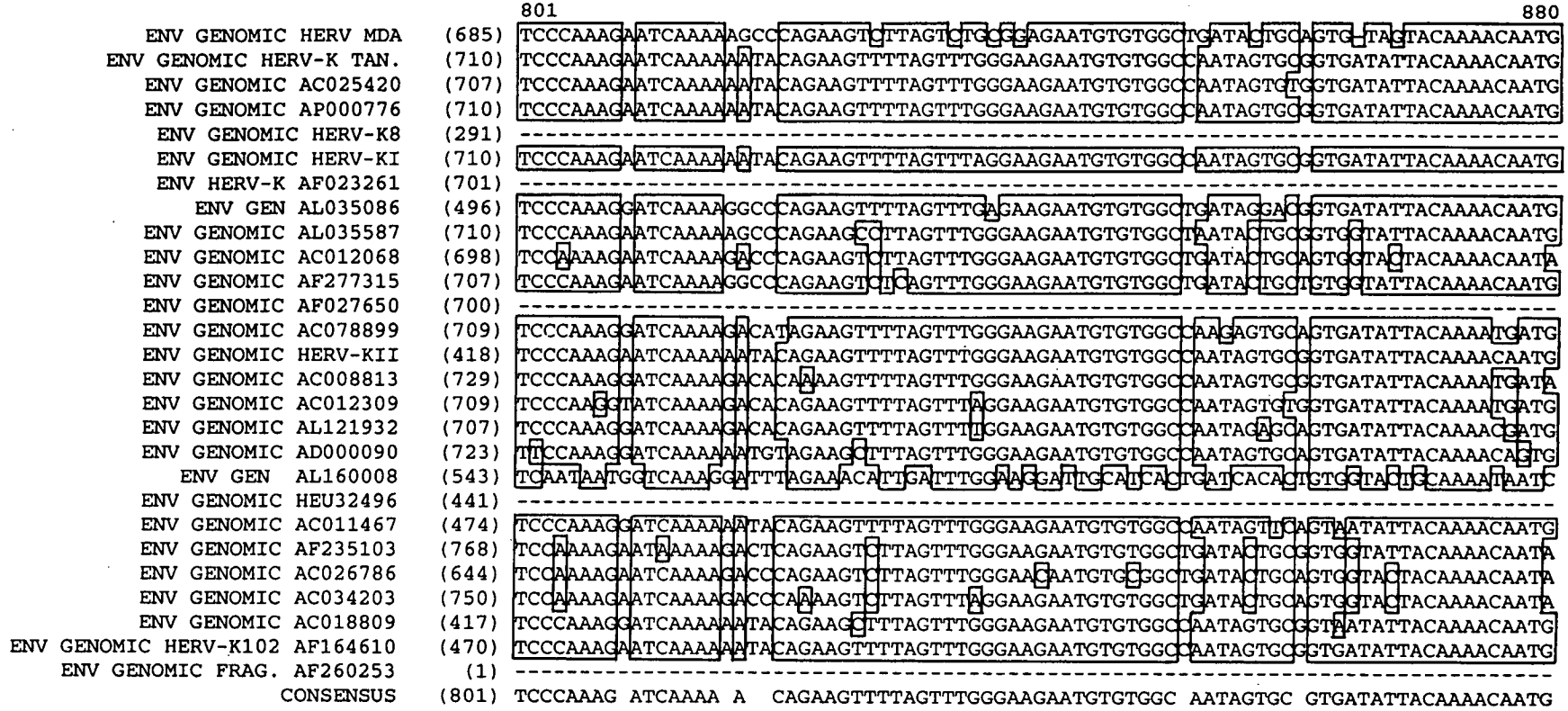
801
880
ENV GENOMIC HERV MDA (685) TCCCAAAGAATCAAAAAGCCCAGAAGTGTTAGTGTGGGAAGAATGTGTGGCTGATAGTGCAGTGGTAGTACAAAACAATG
ENV GENOMIC HERV-K TAN. (710) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
ENV GENOMIC AC025420 (707) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAACAATG
ENV GENOMIC AP000776 (710) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
ENV GENOMIC HERV-K8 (291) ----------
ENV GENOMIC HERV-KI (710) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTAGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
ENV HERV-K AF023261 (701) ----------
ENV GEN AL035086 (496) TCCCAAAGGATCAAAAGGCCCAGAAGTTTTAGTTTGAGAAGAATGTGTGGCTGATAGGACGGTGATATTACAAAACAATG
ENV GENOMIC AL035587 (710) TCCCAAAGAATCAAAAAGCCCAGAAGCGTTAGTTTGGGAAGAATGTGTGGCTAATACTGCGGTGGTATTACAAAACAATG
ENV GENOMIC AC012068 (698) TCCAAAAGAATCAAAAGACCCAGAAGTGTTAGTTTGGGAAGAATGTGTGGCTGATACTGCAGTGGTAGTACAAAACAATA
ENV GENOMIC AF277315 (707) TCCCAAAGAATCAAAAGGCCCAGAAGTGTCAGTTTGGGAAGAATGTGTGGCTGATACTGCGTGTGGTATTACAAAACAATG
ENV GENOMIC AF027650 (700) ----------
ENV GENOMIC AC078899 (709) TCCCAAAGGATCAAAAGACATAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAAGAGTGCAGTGATATTACAAAATGATG
ENV GENOMIC HERV-KII (418) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
ENV GENOMIC AC008813 (729) TCCCAAAGGATCAAAAGACACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAATGATA
ENV GENOMIC AC012309 (709) TCCCAAGGTATCAAAAGACACAGAAGTTTTAGTTTAGGAAGAATGTGTGGCCAATAGTGTGGTGATATTACAAAATGATG
ENV GENOMIC AL121932 (707) TCCCAAAGGATCAAAAGACACAGAAGTTTTAGTTTTGGGAAGAATGTGTGGCCAATAGAGCAGTGATATTACAAAACGATG
ENV GENOMIC AD000090 (723) TTCCAAAGGATCAAAAAATGTAGAAGCTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCAGTGATATTACAAAACAGTG
ENV GEN AL160008 (543) TCAATAATGGTCAAAGGATTTAGAAACATTGATTTGGAAGGATTGCATCAGTGATCACAGTGTGGTACTGCAAAATAATC
ENV GENOMIC HEU32496 (441) ----------
ENV GENOMIC AC011467 (474) TCCCAAAGGATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTTGCAGTAATATTACAAAACAATG
ENV GENOMIC AF235103 (768) TCCAAAAGAATAAAAAGACTCAGAAGTGTTAGTTTGGGAAGAATGTGTGGCTGATACTGCGGTGGTATTACAAAACAATA
ENV GENOMIC AC026786 (644) TCCAAAAGAATCAAAAGACCCAGAAGTGTTAGTTTGGGAAGAATGTGTGGCTGATACTGCAGTGGTACTACAAAACAATA
ENV GENOMIC AC034203 (750) TCCAAAAGAATCAAAAGACCCAAAAGTGTTAGTTTAGGAAGAATGTGTGGCTGATACTGCAGTGGTAGTACAAAACAATA
ENV GENOMIC AC018809 (417) TCCCAAAGGATCAAAAAATACAGAAGCTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTAATATTACAAAACAATG
ENV GENOMIC HERV-K102 AF164610 (470) TCCCAAAGAATCAAAAAATACAGAAGTTTTAGTTTGGGAAGAATGTGTGGCCAATAGTGCGGTGATATTACAAAACAATG
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (801) TCCCAAAG ATCAAAA A CAGAAGTTTTAGTTTGGGAAGAATGTGTGGC AATAGTGC GTGATATTACAAAACAATG

FIG. 6-11

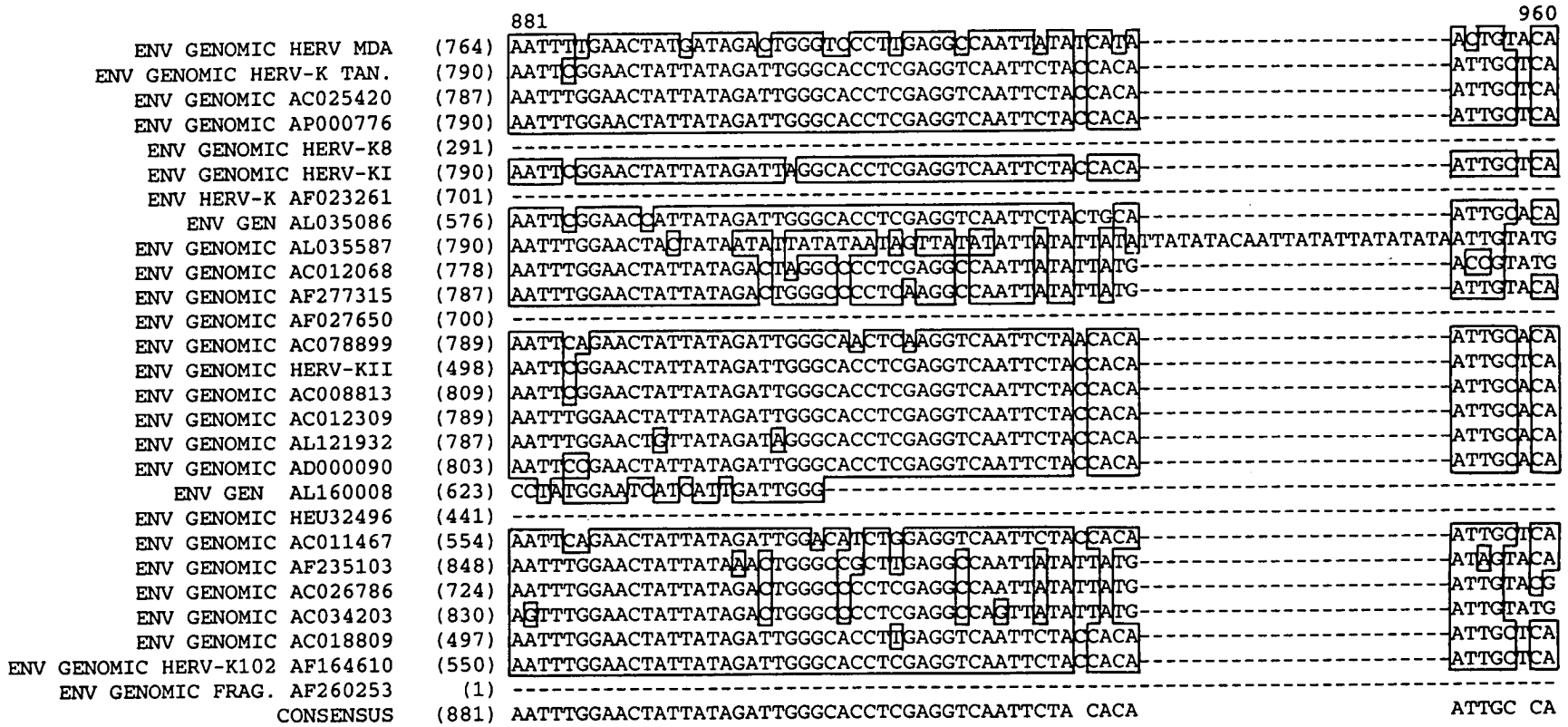
881
960
ENV GENOMIC HERV MDA (764)
ENV GENOMIC HERV-K TAN. (790)
ENV GENOMIC AC025420 (787)
ENV GENOMIC AP000776 (790)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (790)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (576)
ENV GENOMIC AL035587 (790)
ENV GENOMIC AC012068 (778)
ENV GENOMIC AF277315 (787)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (789)
ENV GENOMIC HERV-KII (498)
ENV GENOMIC AC008813 (809)
ENV GENOMIC AC012309 (789)
ENV GENOMIC AL121932 (787)
ENV GENOMIC AD000090 (803)
ENV GEN AL160008 (623)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (554)
ENV GENOMIC AF235103 (848)
ENV GENOMIC AC026786 (724)
ENV GENOMIC AC034203 (830)
ENV GENOMIC AC018809 (497)
ENV GENOMIC HERV-K102 AF164610 (550)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (881) AATTTGGAACTATTATAGATTGGGCACCTCGAGGTCAATTCTA CACA ATTGC CA

FIG. 6-12

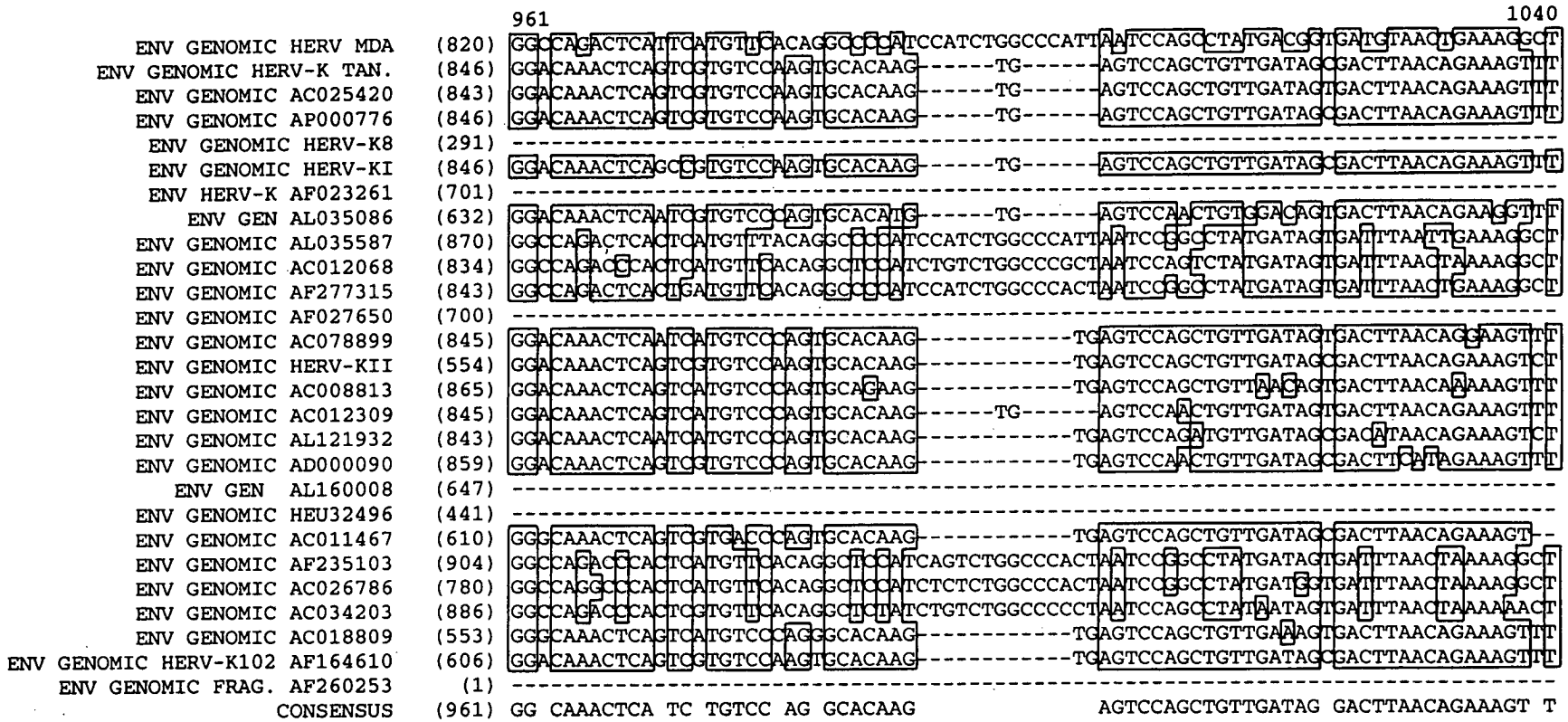
961
1040
ENV GENOMIC HERV MDA (820)
ENV GENOMIC HERV-K TAN. (846)
ENV GENOMIC AC025420 (843)
ENV GENOMIC AP000776 (846)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (846)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (632)
ENV GENOMIC AL035587 (870)
ENV GENOMIC AC012068 (834)
ENV GENOMIC AF277315 (843)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (845)
ENV GENOMIC HERV-KII (554)
ENV GENOMIC AC008813 (865)
ENV GENOMIC AC012309 (845)
ENV GENOMIC AL121932 (843)
ENV GENOMIC AD000090 (859)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (610)
ENV GENOMIC AF235103 (904)
ENV GENOMIC AC026786 (780)
ENV GENOMIC AC034203 (886)
ENV GENOMIC AC018809 (553)
ENV GENOMIC HERV-K102 AF164610 (606)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (961) GG CAAACTCA TC TGTCC AG GCACAAG AGTCCAGCTGTTGATAG GACTTAACAGAAAGT T

FIG. 6-13

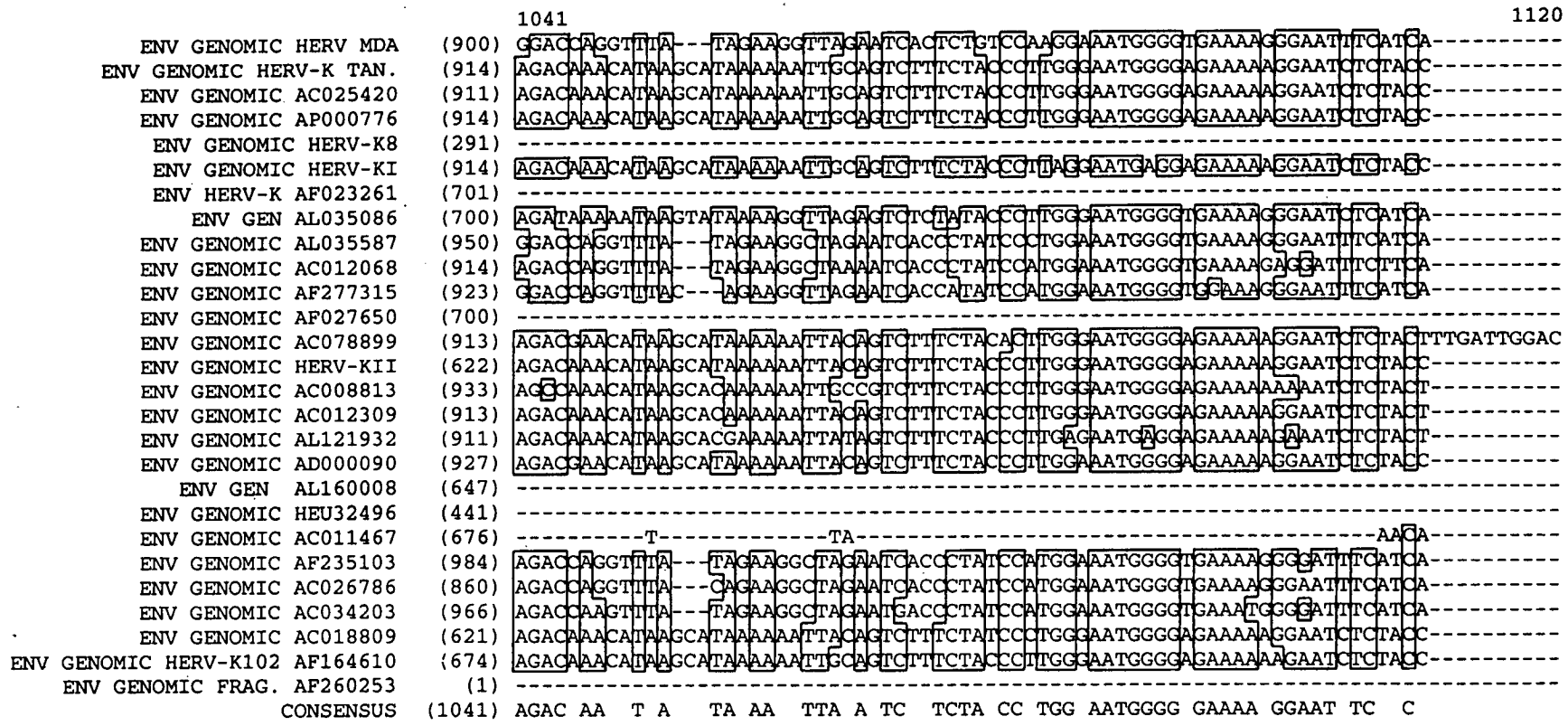
1041
1120
ENV GENOMIC HERV MDA (900)
ENV GENOMIC HERV-K TAN. (914)
ENV GENOMIC AC025420 (911)
ENV GENOMIC AP000776 (914)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (914)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (700)
ENV GENOMIC AL035587 (950)
ENV GENOMIC AC012068 (914)
ENV GENOMIC AF277315 (923)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (913)
ENV GENOMIC HERV-KII (622)
ENV GENOMIC AC008813 (933)
ENV GENOMIC AC012309 (913)
ENV GENOMIC AL121932 (911)
ENV GENOMIC AD000090 (927)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (676)
ENV GENOMIC AF235103 (984)
ENV GENOMIC AC026786 (860)
ENV GENOMIC AC034203 (966)
ENV GENOMIC AC018809 (621)
ENV GENOMIC HERV-K102 AF164610 (674)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1041) AGAC AA T A TA AA TTA A TC TCTA CC TGG AATGGGG GAAAA GGAAT TC C

FIG. 6-14

```
                                          1121                                                                          1200
        ENV GENOMIC HERV MDA     (967) --------------------------------------------------------------------------------
    ENV GENOMIC HERV-K TAN.      (984) --------------------------------------------------------------------------------
        ENV GENOMIC AC025420     (981) --------------------------------------------------------------------------------
        ENV GENOMIC AP000776     (984) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-K8     (291) --------------------------------------------------------------------------------
         ENV GENOMIC HERV-KI     (984) --------------------------------------------------------------------------------
         ENV HERV-K AF023261     (701) --------------------------------------------------------------------------------
            ENV GEN AL035086     (770) --------------------------------------------------------------------------------
        ENV GENOMIC AL035587    (1017) --------------------------------------------------------------------------------
        ENV GENOMIC AC012068     (981) --------------------------------------------------------------------------------
        ENV GENOMIC AF277315     (990) --------------------------------------------------------------------------------
        ENV GENOMIC AF027650     (700) --------------------------------------------------------------------------------
        ENV GENOMIC AC078899     (993) TTCAGCGAAGACTCCAAGATGGCAATCGCCACCTCGGATACCCTAACTCAGCATTTCCGGGTTCACCTTTCCTGTTCCCA
        ENV GENOMIC HERV-KII     (692) --------------------------------------------------------------------------------
        ENV GENOMIC AC008813    (1003) --------------------------------------------------------------------------------
        ENV GENOMIC AC012309     (983) --------------------------------------------------------------------------------
        ENV GENOMIC AL121932     (981) --------------------------------------------------------------------------------
        ENV GENOMIC AD000090     (997) --------------------------------------------------------------------------------
           ENV GEN  AL160008     (647) --------------------------------------------------------------------------------
        ENV GENOMIC HEU32496     (441) --------------------------------------------------------------------------------
        ENV GENOMIC AC011467     (683) --------------------------------------------------------------------------------
        ENV GENOMIC AF235103    (1051) --------------------------------------------------------------------------------
        ENV GENOMIC AC026786     (927) --------------------------------------------------------------------------------
        ENV GENOMIC AC034203    (1033) --------------------------------------------------------------------------------
        ENV GENOMIC AC018809     (691) --------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610   (744) --------------------------------------------------------------------------------
   ENV GENOMIC FRAG. AF260253      (1) --------------------------------------------------------------------------------
                   CONSENSUS    (1121)
```

FIG. 6-15

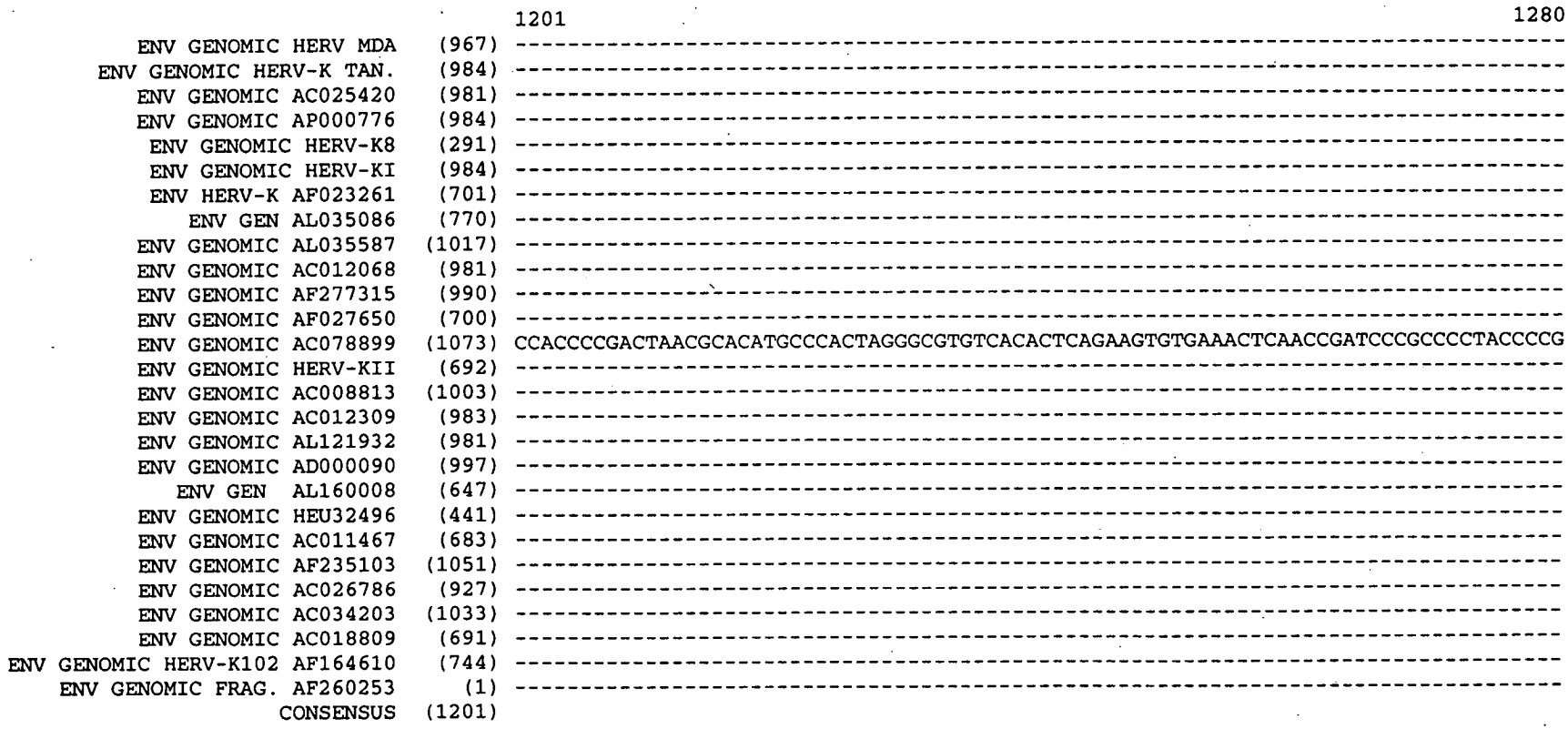
1201
1280
ENV GENOMIC HERV MDA (967)
ENV GENOMIC HERV-K TAN. (984)
ENV GENOMIC AC025420 (981)
ENV GENOMIC AP000776 (984)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (984)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (770)
ENV GENOMIC AL035587 (1017)
ENV GENOMIC AC012068 (981)
ENV GENOMIC AF277315 (990)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1073) CCACCCCGACTAACGCACATGCCCACTAGGGCGTGTCACACTCAGAAGTGTGAAACTCAACCGATCCCGCCCCTACCCCG
ENV GENOMIC HERV-KII (692)
ENV GENOMIC AC008813 (1003)
ENV GENOMIC AC012309 (983)
ENV GENOMIC AL121932 (981)
ENV GENOMIC AD000090 (997)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (683)
ENV GENOMIC AF235103 (1051)
ENV GENOMIC AC026786 (927)
ENV GENOMIC AC034203 (1033)
ENV GENOMIC AC018809 (691)
ENV GENOMIC HERV-K102 AF164610 (744)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1201)

FIG. 6-16

```
                                        1281                                                                        1360
          ENV GENOMIC HERV MDA    (967) ------------------------------------------------------------------------------------------
        ENV GENOMIC HERV-K TAN.   (984) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC025420    (981) ------------------------------------------------------------------------------------------
          ENV GENOMIC AP000776    (984) ------------------------------------------------------------------------------------------
           ENV GENOMIC HERV-K8    (291) ------------------------------------------------------------------------------------------
           ENV GENOMIC HERV-KI    (984) ------------------------------------------------------------------------------------------
           ENV HERV-K AF023261    (701) ------------------------------------------------------------------------------------------
              ENV GEN AL035086    (770) ------------------------------------------------------------------------------------------
          ENV GENOMIC AL035587   (1017) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC012068    (981) ------------------------------------------------------------------------------------------
          ENV GENOMIC AF277315    (990) ------------------------------------------------------------------------------------------
          ENV GENOMIC AF027650    (700) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC078899   (1153) ACCACTCCTCACCCAGCATCCATAAAAGCGCGCTGCACCTTTCGCACAGCGTGACTTCCCCTGGCGGACCAGTGAACCTC
          ENV GENOMIC HERV-KII    (692) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC008813   (1003) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC012309    (983) ------------------------------------------------------------------------------------------
          ENV GENOMIC AL121932    (981) ------------------------------------------------------------------------------------------
          ENV GENOMIC AD000090    (997) ------------------------------------------------------------------------------------------
             ENV GEN  AL160008    (647) ------------------------------------------------------------------------------------------
          ENV GENOMIC HEU32496    (441) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC011467    (683) ------------------------------------------------------------------------------------------
          ENV GENOMIC AF235103   (1051) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC026786    (927) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC034203   (1033) ------------------------------------------------------------------------------------------
          ENV GENOMIC AC018809    (691) ------------------------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610    (744) ------------------------------------------------------------------------------------------
    ENV GENOMIC FRAG. AF260253      (1) ------------------------------------------------------------------------------------------
                      CONSENSUS (1281)
```

FIG. 6-17

```
                                        1361                                                                1440
      ENV GENOMIC HERV MDA    (967) ----------------------------------------------------------------------------
   ENV GENOMIC HERV-K TAN.    (984) ----------------------------------------------------------------------------
      ENV GENOMIC AC025420    (981) ----------------------------------------------------------------------------
      ENV GENOMIC AP000776    (984) ----------------------------------------------------------------------------
       ENV GENOMIC HERV-K8    (291) ----------------------------------------------------------------------------
       ENV GENOMIC HERV-KI    (984) ----------------------------------------------------------------------------
       ENV HERV-K AF023261    (701) ----------------------------------------------------------------------------
          ENV GEN AL035086    (770) ----------------------------------------------------------------------------
      ENV GENOMIC AL035587   (1017) ----------------------------------------------------------------------------
      ENV GENOMIC AC012068    (981) ----------------------------------------------------------------------------
      ENV GENOMIC AF277315    (990) ----------------------------------------------------------------------------
      ENV GENOMIC AF027650    (700) ----------------------------------------------------------------------------
      ENV GENOMIC AC078899   (1233) ACCGGAGAGCTCAATAAAGAAGATTTTTGCCCTCTTTGTCTTGCCTCTTGGCCTTATTGATCCACGGTGCCTTTCCATTG
      ENV GENOMIC HERV-KII    (692) ----------------------------------------------------------------------------
      ENV GENOMIC AC008813   (1003) ----------------------------------------------------------------------------
      ENV GENOMIC AC012309    (983) ----------------------------------------------------------------------------
      ENV GENOMIC AL121932    (981) ----------------------------------------------------------------------------
      ENV GENOMIC AD000090    (997) ----------------------------------------------------------------------------
         ENV GEN  AL160008    (647) ----------------------------------------------------------------------------
      ENV GENOMIC HEU32496    (441) ----------------------------------------------------------------------------
      ENV GENOMIC AC011467    (683) ----------------------------------------------------------------------------
      ENV GENOMIC AF235103   (1051) ----------------------------------------------------------------------------
      ENV GENOMIC AC026786    (927) ----------------------------------------------------------------------------
      ENV GENOMIC AC034203   (1033) ----------------------------------------------------------------------------
      ENV GENOMIC AC018809    (691) ----------------------------------------------------------------------------
ENV GENOMIC HERV-K102 AF164610    (744) ----------------------------------------------------------------------------
    ENV GENOMIC FRAG. AF260253      (1) ----------------------------------------------------------------------------
                    CONSENSUS   (1361)
```

FIG. 6-18

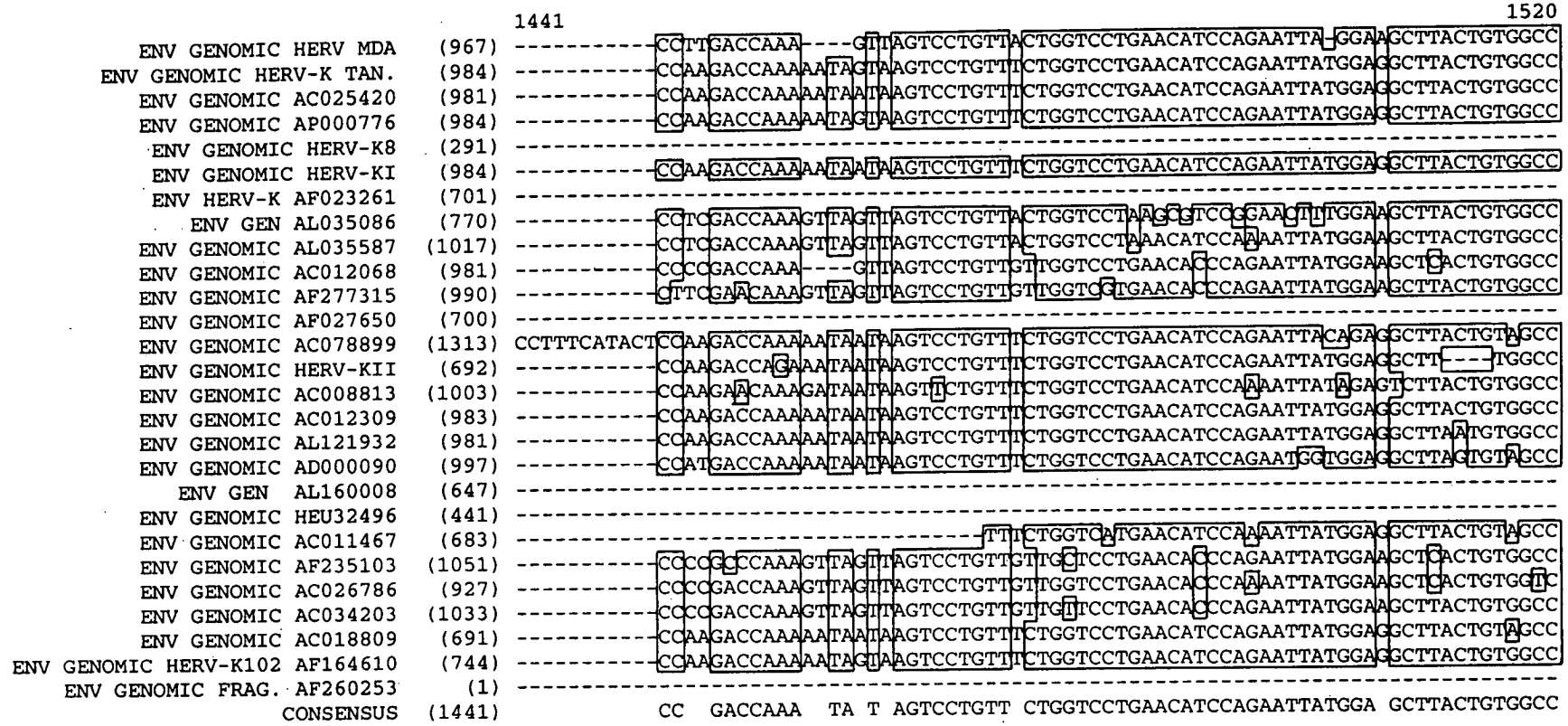
1441
1520
ENV GENOMIC HERV MDA (967)
ENV GENOMIC HERV-K TAN. (984)
ENV GENOMIC AC025420 (981)
ENV GENOMIC AP000776 (984)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (984)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (770)
ENV GENOMIC AL035587 (1017)
ENV GENOMIC AC012068 (981)
ENV GENOMIC AF277315 (990)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1313)
ENV GENOMIC HERV-KII (692)
ENV GENOMIC AC008813 (1003)
ENV GENOMIC AC012309 (983)
ENV GENOMIC AL121932 (981)
ENV GENOMIC AD000090 (997)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (683)
ENV GENOMIC AF235103 (1051)
ENV GENOMIC AC026786 (927)
ENV GENOMIC AC034203 (1033)
ENV GENOMIC AC018809 (691)
ENV GENOMIC HERV-K102 AF164610 (744)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1441)
CC GACCAAA TA T AGTCCTGTT CTGGTCCTGAACATCCAGAATTATGGA GCTTACTGTGGCC

FIG. 6-19

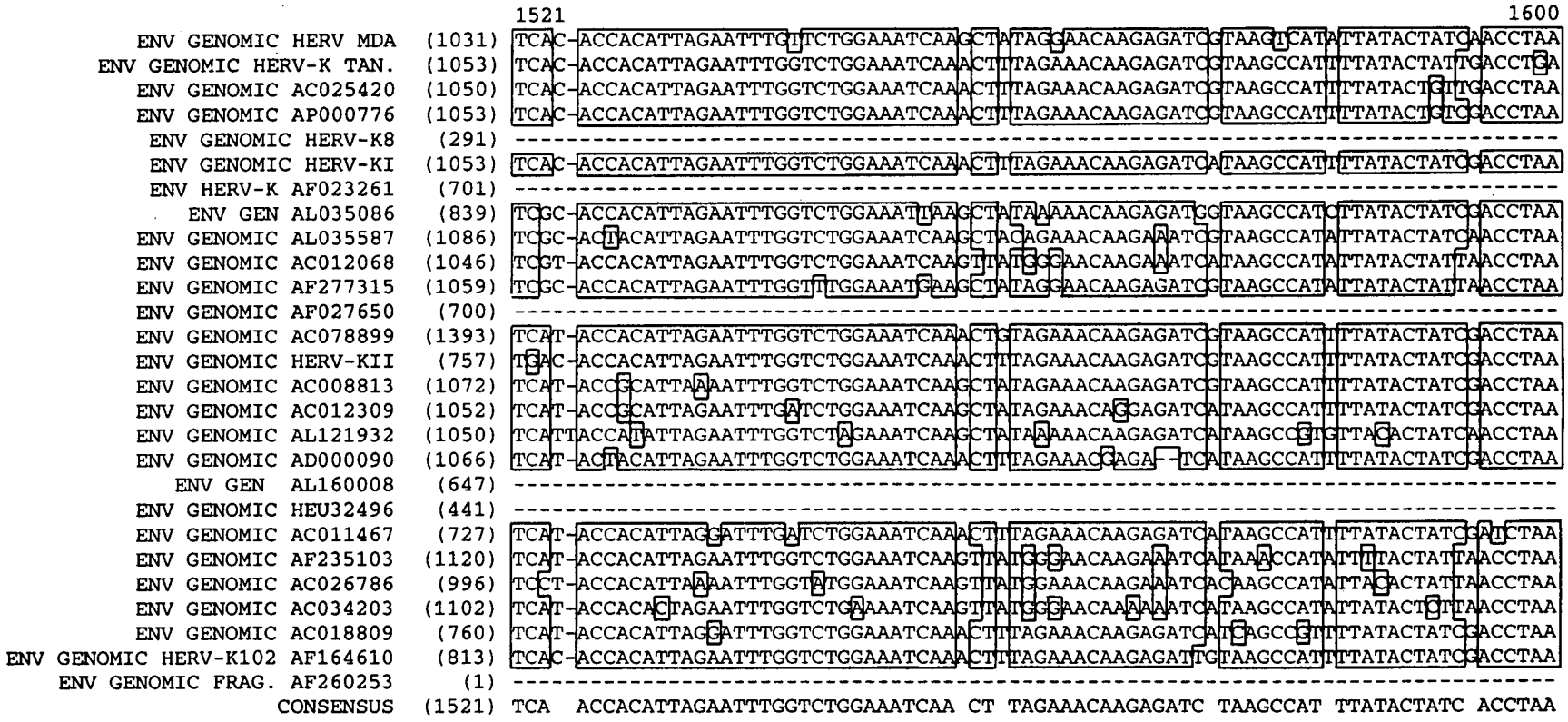
1521
1600
ENV GENOMIC HERV MDA (1031)
ENV GENOMIC HERV-K TAN. (1053)
ENV GENOMIC AC025420 (1050)
ENV GENOMIC AP000776 (1053)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1053)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (839)
ENV GENOMIC AL035587 (1086)
ENV GENOMIC AC012068 (1046)
ENV GENOMIC AF277315 (1059)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1393)
ENV GENOMIC HERV-KII (757)
ENV GENOMIC AC008813 (1072)
ENV GENOMIC AC012309 (1052)
ENV GENOMIC AL121932 (1050)
ENV GENOMIC AD000090 (1066)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (727)
ENV GENOMIC AF235103 (1120)
ENV GENOMIC AC026786 (996)
ENV GENOMIC AC034203 (1102)
ENV GENOMIC AC018809 (760)
ENV GENOMIC HERV-K102 AF164610 (813)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1521) TCA ACCACATTAGAATTTGGTCTGGAAATCAA CT TAGAAACAAGAGATC TAAGCCAT TTATACTATC ACCTAA

FIG. 6-20

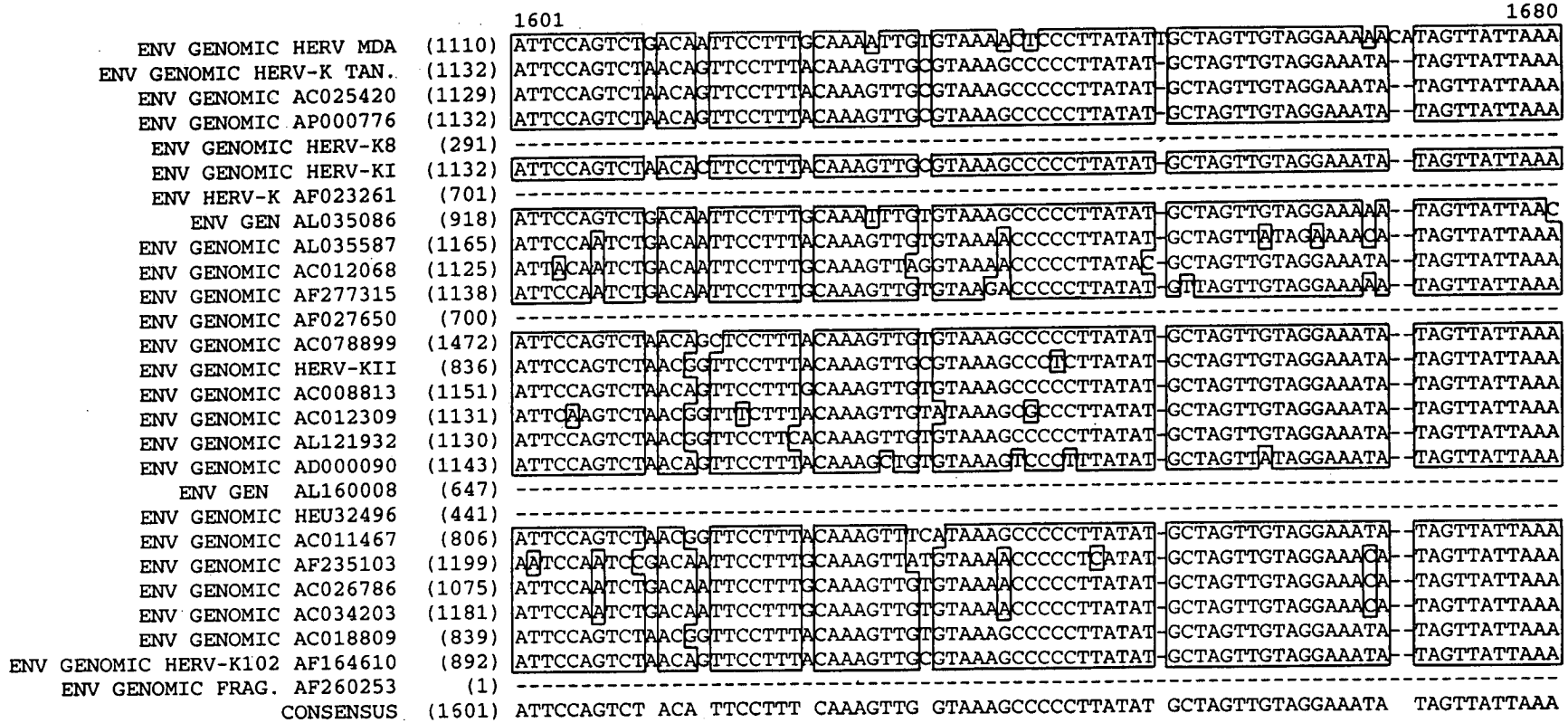
1601
1680
ENV GENOMIC HERV MDA (1110) ATTCCAGTCTGACAATTCCTTTGCAAAATTGTGTAAAACCCCCTTATATTGCTAGTTGTAGGAAAAACATAGTTATTAAA
ENV GENOMIC HERV-K TAN. (1132) ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AC025420 (1129) ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AP000776 (1132) ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC HERV-K8 (291) ----------
ENV GENOMIC HERV-KI (1132) ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV HERV-K AF023261 (701) ----------
ENV GEN AL035086 (918) ATTCCAGTCTGACAATTCCTTTGCAAATTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAAAA--TAGTTATTAAC
ENV GENOMIC AL035587 (1165) ATTCCAATCTGACAATTCCTTTACAAAGTTGTGTAAAACCCCCTTATAT-GCTAGTTTATAGAAAACA--TAGTTATTAAA
ENV GENOMIC AC012068 (1125) ATTACAATCTGACAATTCCTTTGCAAAGTTAGGTAAAACCCCCTTATAC-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AF277315 (1138) ATTCCAATCTGACAATTCCTTTGCAAAGTTGTGTAAGACCCCCTTATAT-GTTAGTTGTAGGAAAAA--TAGTTATTAAA
ENV GENOMIC AF027650 (700) ----------
ENV GENOMIC AC078899 (1472) ATTCCAGTCTAACAGCTCCTTTACAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC HERV-KII (836) ATTCCAGTCTAACGGTTCCTTTACAAAGTTGCGTAAAGCCCTCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AC008813 (1151) ATTCCAGTCTAACAGTTCCTTTGCAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AC012309 (1131) ATTCAAGTCTAACGGTTTCTTTACAAAGTTGTATAAAGCGCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AL121932 (1130) ATTCCAGTCTAACGGTTCCTTCACAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AD000090 (1143) ATTCCAGTCTAACAGTTCCTTTACAAAGCTGTGTAAAGTCCGTTTATAT-GCTAGTTATAGGAAATA--TAGTTATTAAA
ENV GEN AL160008 (647) ----------
ENV GENOMIC HEU32496 (441) ----------
ENV GENOMIC AC011467 (806) ATTCCAGTCTAACGGTTCCTTTACAAAGTTTCATAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC AF235103 (1199) AATCCAATCCGACAATTCCTTTGCAAAGTTATGTAAAACCCCCTCATAT-GCTAGTTGTAGGAAACA--TAGTTATTAAA
ENV GENOMIC AC026786 (1075) ATTCCAATCTGACAATTCCTTTGCAAAGTTGTGTAAAACCCCCTTATAT-GCTAGTTGTAGGAAACA--TAGTTATTAAA
ENV GENOMIC AC034203 (1181) ATTCCAATCTGACAATTCCTTTGCAAAGTTGTGTAAAACCCCCTTATAT-GCTAGTTGTAGGAAACA--TAGTTATTAAA
ENV GENOMIC AC018809 (839) ATTCCAGTCTAACGGTTCCTTTACAAAGTTGTGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC HERV-K102 AF164610 (892) ATTCCAGTCTAACAGTTCCTTTACAAAGTTGCGTAAAGCCCCCTTATAT-GCTAGTTGTAGGAAATA--TAGTTATTAAA
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (1601) ATTCCAGTCT ACA TTCCTTT CAAAGTTG GTAAAGCCCCCTTATAT GCTAGTTGTAGGAAATA TAGTTATTAAA

FIG. 6-21

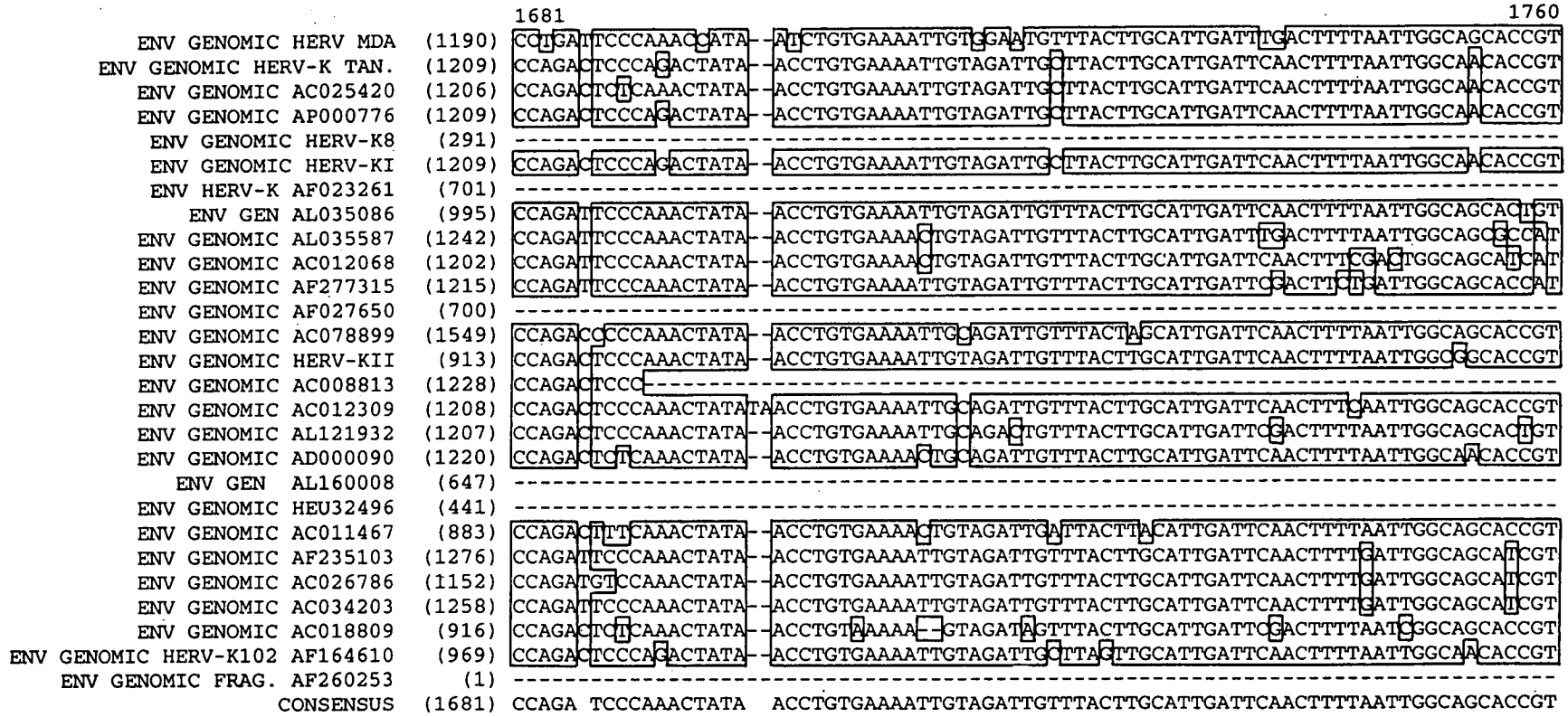
1681
1760
ENV GENOMIC HERV MDA (1190)
ENV GENOMIC HERV-K TAN. (1209)
ENV GENOMIC AC025420 (1206)
ENV GENOMIC AP000776 (1209)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1209)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (995)
ENV GENOMIC AL035587 (1242)
ENV GENOMIC AC012068 (1202)
ENV GENOMIC AF277315 (1215)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1549)
ENV GENOMIC HERV-KII (913)
ENV GENOMIC AC008813 (1228)
ENV GENOMIC AC012309 (1208)
ENV GENOMIC AL121932 (1207)
ENV GENOMIC AD000090 (1220)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (883)
ENV GENOMIC AF235103 (1276)
ENV GENOMIC AC026786 (1152)
ENV GENOMIC AC034203 (1258)
ENV GENOMIC AC018809 (916)
ENV GENOMIC HERV-K102 AF164610 (969)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1681) CCAGA TCCCAAACTATA ACCTGTGAAAATTGTAGATTGTTTACTTGCATTGATTCAACTTTTAATTGGCAGCACCGT

FIG. 6-22

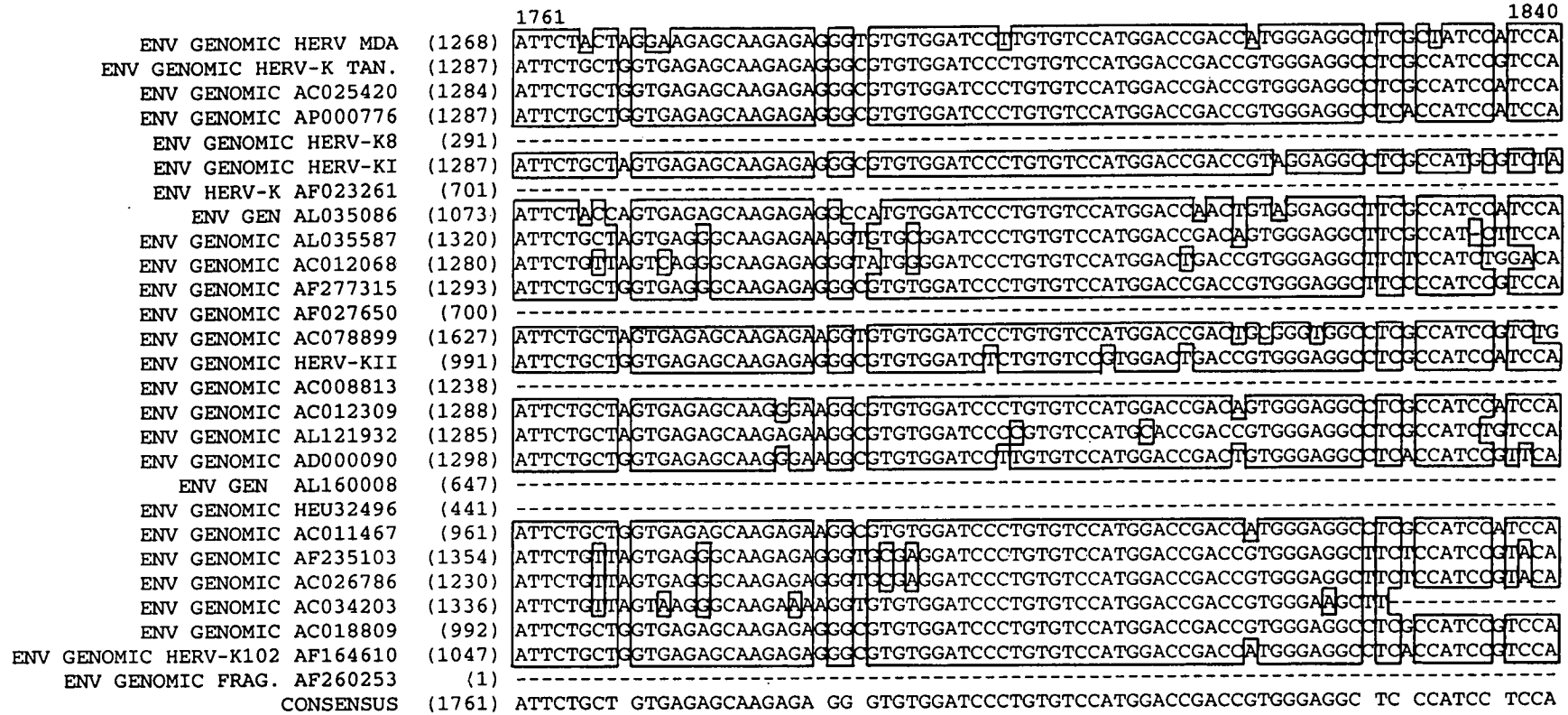
1761
1840
ENV GENOMIC HERV MDA (1268) ATTCTACTAGGAAGAGCAAGAGAGGGTGTGTGGATCCTTGTGTCCATGGACCGACCATGGGAGGCTTCGCTATCCATCCA
ENV GENOMIC HERV-K TAN. (1287) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCCGTCCA
ENV GENOMIC AC025420 (1284) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCCATCCA
ENV GENOMIC AP000776 (1287) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCACCATCCATCCA
ENV GENOMIC HERV-K8 (291) ----------
ENV GENOMIC HERV-KI (1287) ATTCTGCTAGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTAGGAGGCCTCGCCATGGGTCTA
ENV HERV-K AF023261 (701) ----------
ENV GEN AL035086 (1073) ATTCTACCAGTGAGAGCAAGAGAGGCCATGTGGATCCCTGTGTCCATGGACCAACTGTAGGAGGCTTCGCCATCCATCCA
ENV GENOMIC AL035587 (1320) ATTCTGCTAGTGAGGGCAAGAGAAGGTGTGCGGATCCCTGTGTCCATGGACCGACAGTGGGAGGCTTCGCCATCGTTCCA
ENV GENOMIC AC012068 (1280) ATTCTGTTAGTCAGGGCAAGAGAGGGTATGGGGATCCCTGTGTCCATGGACTGACCGTGGGAGGCTTCTCCATCTGGACA
ENV GENOMIC AF277315 (1293) ATTCTGCTGGTGAGGGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCTTCCCCATCCGTCCA
ENV GENOMIC AF027650 (700) ----------
ENV GENOMIC AC078899 (1627) ATTCTGCTAGTGAGAGCAAGAGAAGGTGTGTGGATCCCTGTGTCCATGGACCGACTGCGGGTGGCCTCGCCATCCGTCTG
ENV GENOMIC HERV-KII (991) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCTCTGTGTCCGTGGACTGACCGTGGGAGGCCTCGCCATCCATCCA
ENV GENOMIC AC008813 (1238) ----------
ENV GENOMIC AC012309 (1288) ATTCTGCTAGTGAGAGCAAGGGAAGGCGTGTGGATCCCTGTGTCCATGGACCGACAGTGGGAGGCCTCGCCATCCATCCA
ENV GENOMIC AL121932 (1285) ATTCTGCTAGTGAGAGCAAGAGAAGGCGTGTGGATCCCCGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCTGTCCA
ENV GENOMIC AD000090 (1298) ATTCTGCTGGTGAGAGCAAGGGAAGGCGTGTGGATCCTTGTGTCCATGGACCGACTGTGGGAGGCCTCACCATCCGTTCA
ENV GEN AL160008 (647) ----------
ENV GENOMIC HEU32496 (441) ----------
ENV GENOMIC AC011467 (961) ATTCTGCTGGTGAGAGCAAGAGAAGGCGTGTGGATCCCTGTGTCCATGGACCGACCATGGGAGGCCTCGCCATCCATCCA
ENV GENOMIC AF235103 (1354) ATTCTGTTAGTGAGGGCAAGAGAGGGTGCGAGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCTTCTCCATCCGTACA
ENV GENOMIC AC026786 (1230) ATTCTGTTAGTGAGGGCAAGAGAGGGTGCGAGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCTTCTCCATCCGTACA
ENV GENOMIC AC034203 (1336) ATTCTGTTAGTAAGGGCAAGAAAAGGTGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAAGCTTC----------
ENV GENOMIC AC018809 (992) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGCCTCGCCATCCGTCCA
ENV GENOMIC HERV-K102 AF164610 (1047) ATTCTGCTGGTGAGAGCAAGAGAGGGCGTGTGGATCCCTGTGTCCATGGACCGACCATGGGAGGCCTCACCATCCGTCCA
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (1761) ATTCTGCT GTGAGAGCAAGAGA GG GTGTGGATCCCTGTGTCCATGGACCGACCGTGGGAGGC TC CCATCC TCCA

FIG. 6-23

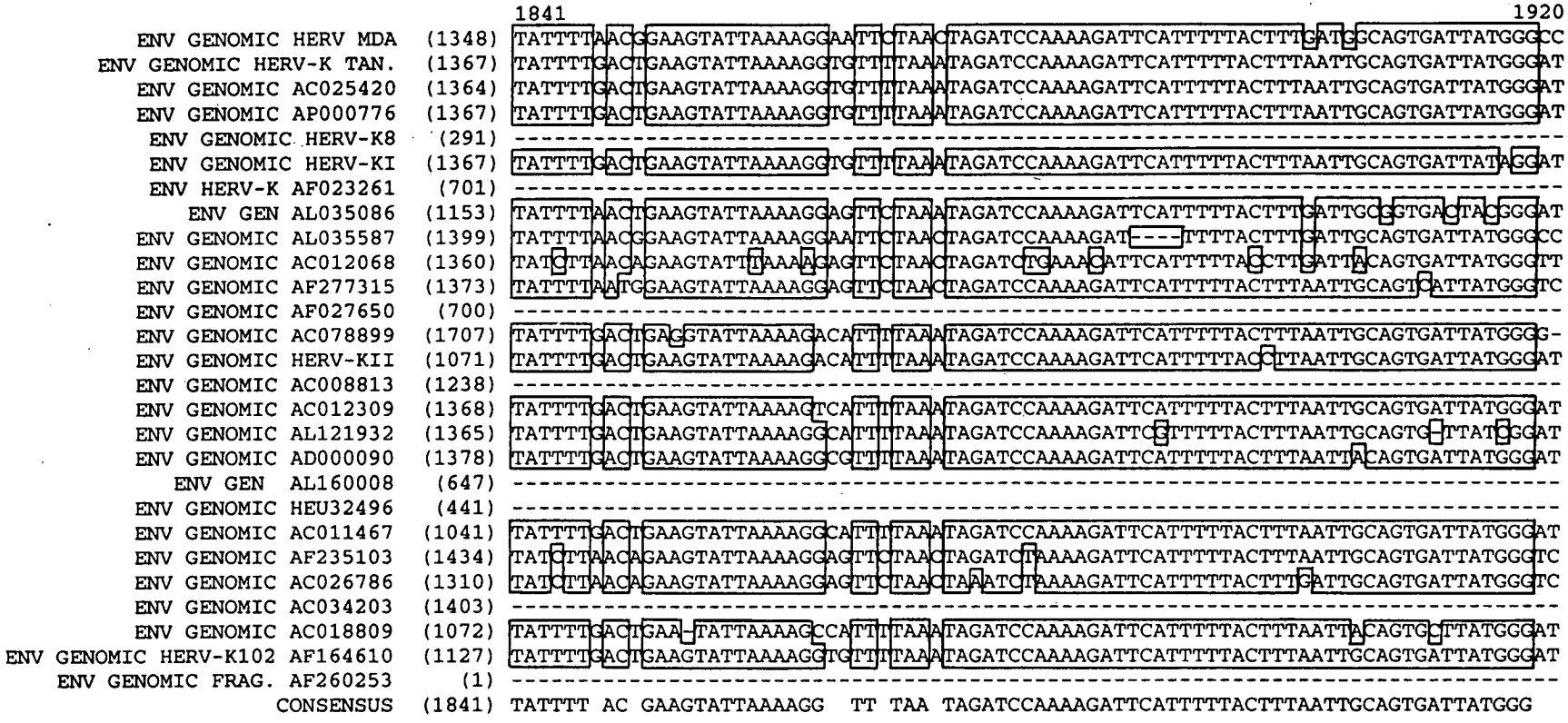
1841
1920
ENV GENOMIC HERV MDA (1348) TATTTTAACGGAAGTATTAAAAGGAATTCTAACTAGATCCAAAAGATTCATTTTTACTTTGATGGCAGTGATTATGGGCC
ENV GENOMIC HERV-K TAN. (1367) TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
ENV GENOMIC AC025420 (1364) TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
ENV GENOMIC AP000776 (1367) TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1367) TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATAGGAT
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1153) TATTTTAACTGAAGTATTAAAAGGAGTTCTAAATAGATCCAAAAGATTCATTTTTACTTTGATTGCGGTGAGTACGGGAT
ENV GENOMIC AL035587 (1399) TATTTTAACGGAAGTATTAAAAGGAATTCTAACTAGATCCAAAAGAT----TTTTACTTTGATTGCAGTGATTATGGGCC
ENV GENOMIC AC012068 (1360) TATGTTAACAGAAGTATTTAAAAGAGTTCTAACTAGATCTGAAAGATTCATTTTTAGCTTGATTACAGTGATTATGGGTT
ENV GENOMIC AF277315 (1373) TATTTTAATGGAAGTATTAAAAGGAGTTCTAACTAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGTC
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1707) TATTTTGACTGAGGTATTAAAAGACATTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGG-
ENV GENOMIC HERV-KII (1071) TATTTTGACTGAAGTATTAAAAGACATTTTTAAATAGATCCAAAAGATTCATTTTTAGCTTAATTGCAGTGATTATGGGAT
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1368) TATTTTGACTGAAGTATTAAAAGTCATTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
ENV GENOMIC AL121932 (1365) TATTTTGACTGAAGTATTAAAAGGCATTTTTAAATAGATCCAAAAGATTCGTTTTTACTTTAATTGCAGTGTTTATTGGGAT
ENV GENOMIC AD000090 (1378) TATTTTGACTGAAGTATTAAAAGGCGTTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTACAGTGATTATGGGAT
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1041) TATTTTGACTGAAGTATTAAAAGGCATTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
ENV GENOMIC AF235103 (1434) TATGTTAACAGAAGTATTAAAAGGAGTTCTAACTAGATCTAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGTC
ENV GENOMIC AC026786 (1310) TATGTTAACAGAAGTATTAAAAGGAGTTCTAACTAAATCTAAAAGATTCATTTTTACTTTGATTGCAGTGATTATGGGTC
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1072) TATTTTGACTGAA-TATTAAAAGCCATTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTACAGTGGTTATGGGAT
ENV GENOMIC HERV-K102 AF164610 (1127) TATTTTGACTGAAGTATTAAAAGGTGTTTTAAATAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGGAT
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1841) TATTTT AC GAAGTATTAAAAGG TT TAA TAGATCCAAAAGATTCATTTTTACTTTAATTGCAGTGATTATGGG

FIG. 6-24

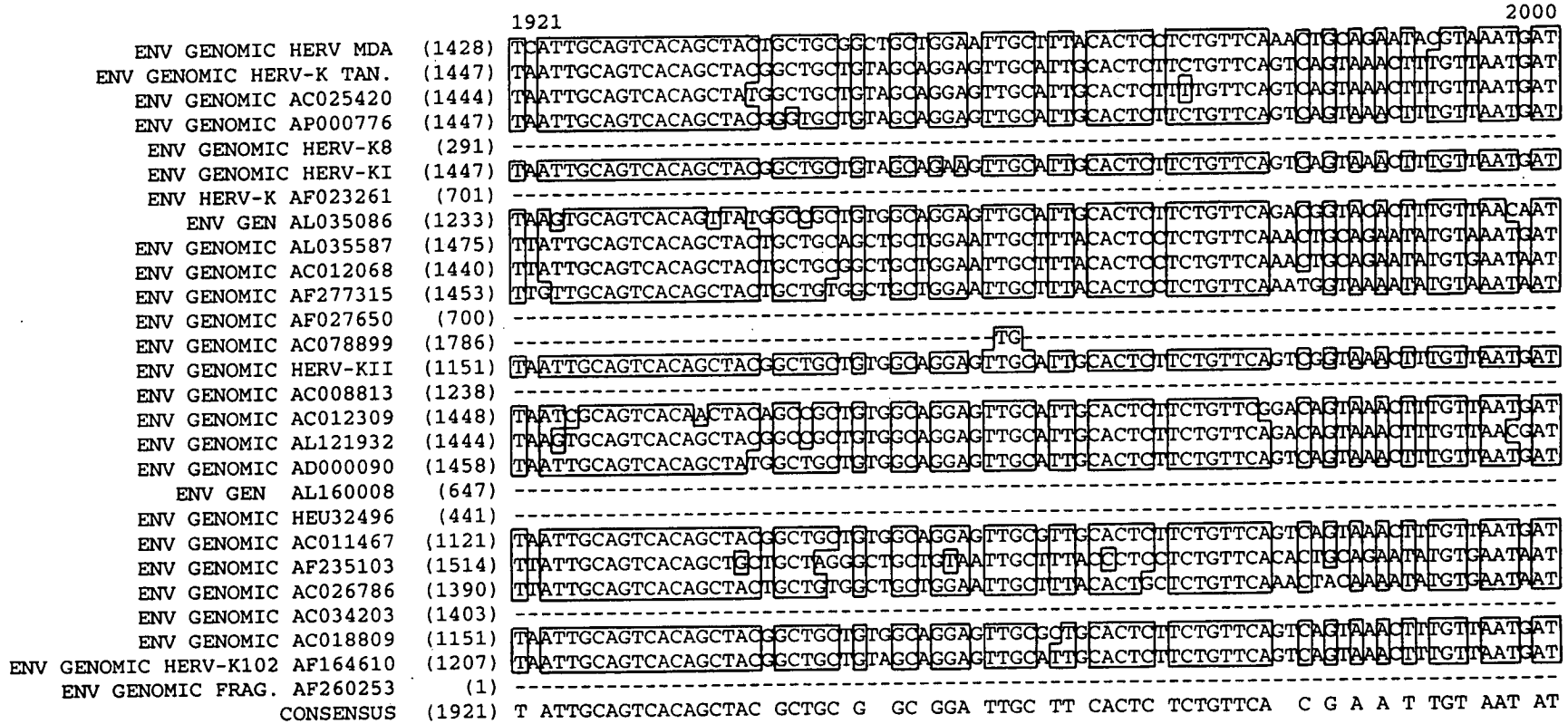
1921
2000
ENV GENOMIC HERV MDA (1428)
ENV GENOMIC HERV-K TAN. (1447)
ENV GENOMIC AC025420 (1444)
ENV GENOMIC AP000776 (1447)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1447)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1233)
ENV GENOMIC AL035587 (1475)
ENV GENOMIC AC012068 (1440)
ENV GENOMIC AF277315 (1453)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1786)
ENV GENOMIC HERV-KII (1151)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1448)
ENV GENOMIC AL121932 (1444)
ENV GENOMIC AD000090 (1458)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1121)
ENV GENOMIC AF235103 (1514)
ENV GENOMIC AC026786 (1390)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1151)
ENV GENOMIC HERV-K102 AF164610 (1207)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (1921) T ATTGCAGTCACAGCTAC GCTGC G GC GGA TTGC TT CACTC TCTGTTCA C G A A T TGT AAT AT

FIG. 6-25

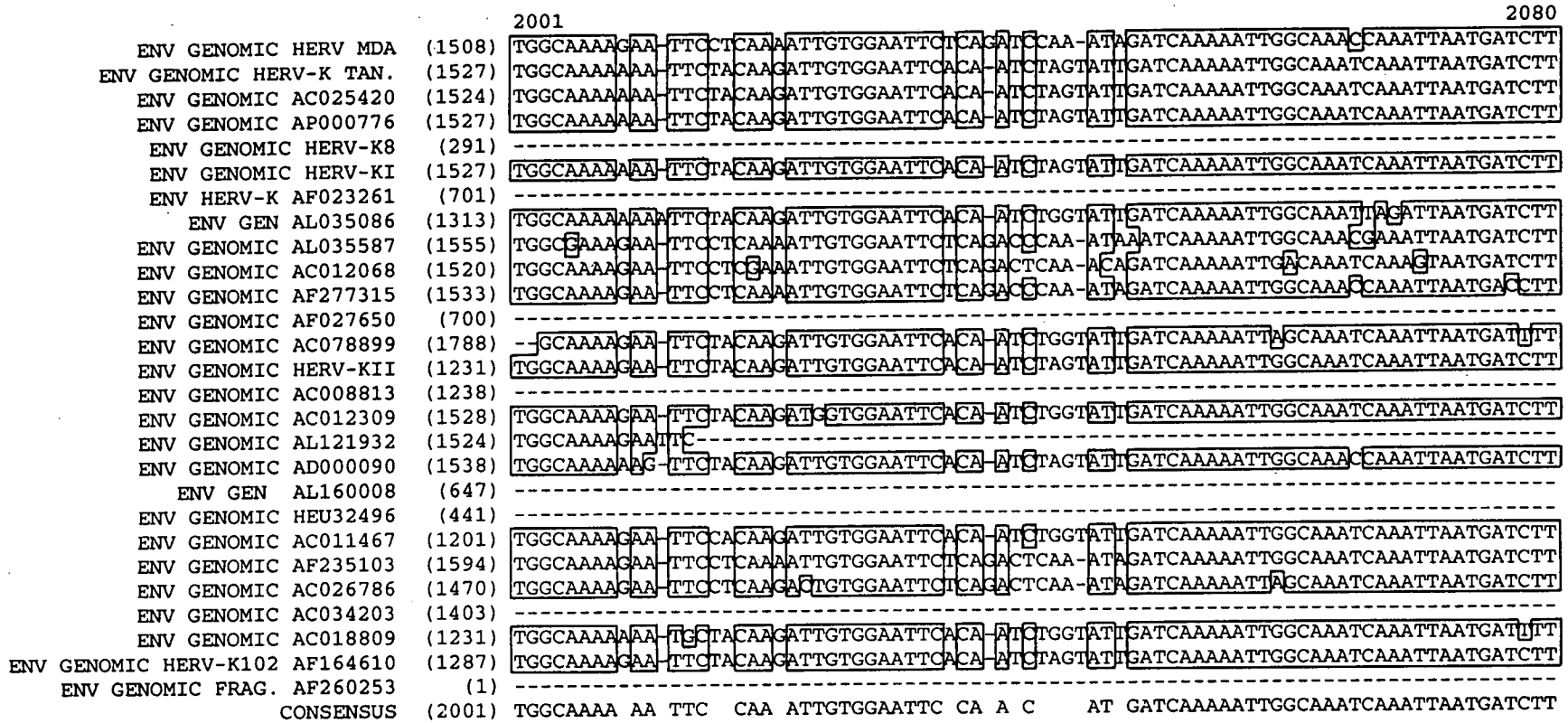
2001
2080
ENV GENOMIC HERV MDA (1508)
ENV GENOMIC HERV-K TAN. (1527)
ENV GENOMIC AC025420 (1524)
ENV GENOMIC AP000776 (1527)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1527)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1313)
ENV GENOMIC AL035587 (1555)
ENV GENOMIC AC012068 (1520)
ENV GENOMIC AF277315 (1533)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1788)
ENV GENOMIC HERV-KII (1231)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1528)
ENV GENOMIC AL121932 (1524)
ENV GENOMIC AD000090 (1538)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1201)
ENV GENOMIC AF235103 (1594)
ENV GENOMIC AC026786 (1470)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1231)
ENV GENOMIC HERV-K102 AF164610 (1287)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (2001) TGGCAAAA AA TTC CAA ATTGTGGAATTC CA A C AT GATCAAAAATTGGCAAATCAAATTAATGATCTT

FIG. 6-26

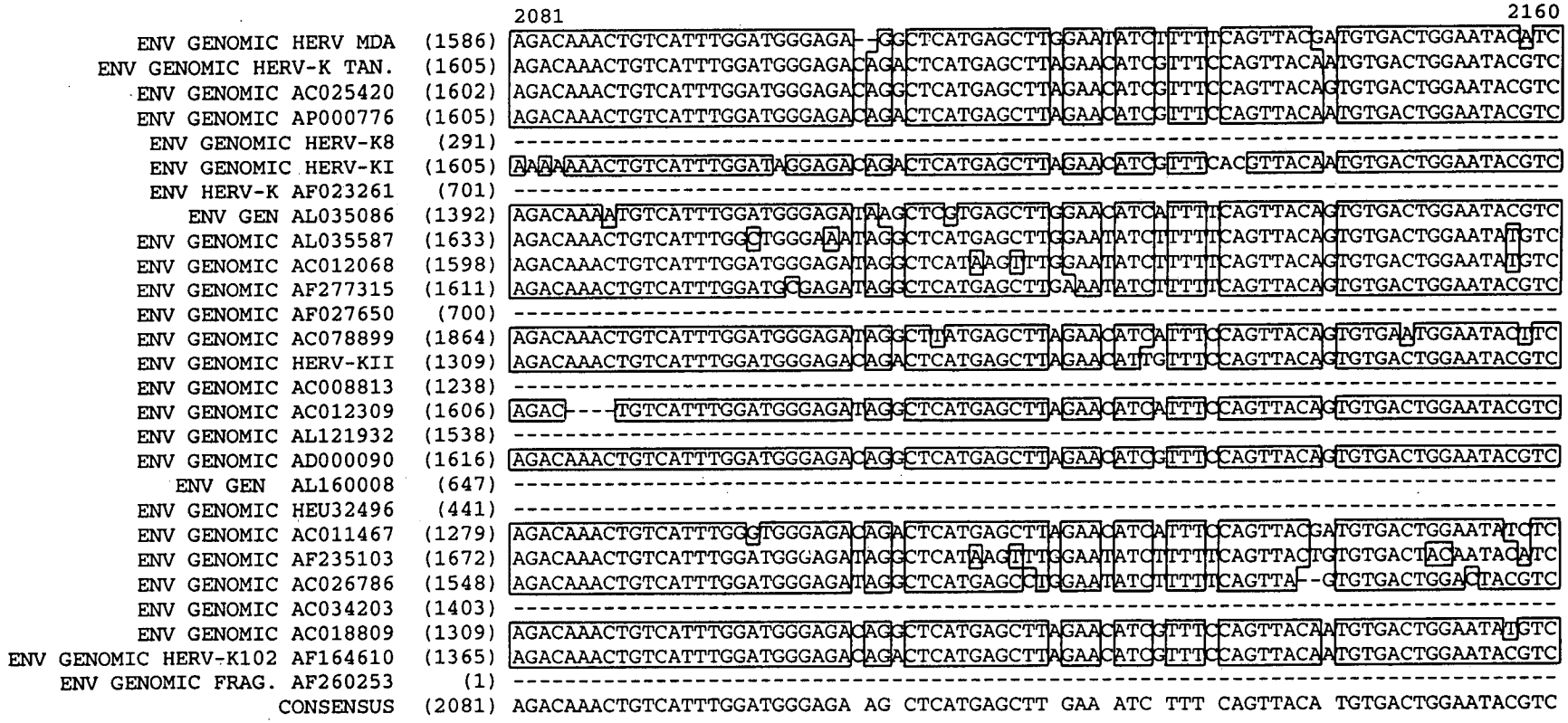
2081
2160
ENV GENOMIC HERV MDA (1586) AGACAAACTGTCATTTGGATGGGAGA--GGCTCATGAGCTTGGAATATCTTTTTCAGTTACGATGTGACTGGAATACATC
ENV GENOMIC HERV-K TAN. (1605) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTC
ENV GENOMIC AC025420 (1602) AGACAAACTGTCATTTGGATGGGAGACAGGCTCATGAGCTTAGAACATCGTTTCCAGTTACAGTGTGACTGGAATACGTC
ENV GENOMIC AP000776 (1605) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTC
ENV GENOMIC HERV-K8 (291) ----------
ENV GENOMIC HERV-KI (1605) AAAAAAACTGTCATTTGGATAGGAGACAGACTCATGAGCTTAGAACATCGTTTCACGTTACAATGTGACTGGAATACGTC
ENV HERV-K AF023261 (701) ----------
ENV GEN AL035086 (1392) AGACAAAATGTCATTTGGATGGGAGATAAGCTCGTGAGCTTGGAACATCATTTTCAGTTACAGTGTGACTGGAATACGTC
ENV GENOMIC AL035587 (1633) AGACAAACTGTCATTTGGCTGGGAAATAGGCTCATGAGCTTGGAATATCTTTTTCAGTTACAGTGTGACTGGAATATGTC
ENV GENOMIC AC012068 (1598) AGACAAACTGTCATTTGGATGGGAGATAGGCTCATAAGTTTGGAATATCTTTTTCAGTTACAGTGTGACTGGAATATGTC
ENV GENOMIC AF277315 (1611) AGACAAACTGTCATTTGGATGCGAGATAGGCTCATGAGCTTGAAATATCTTTTTCAGTTACAGTGTGACTGGAATACGTC
ENV GENOMIC AF027650 (700) ----------
ENV GENOMIC AC078899 (1864) AGACAAACTGTCATTTGGATGGGAGATAGGCTTATGAGCTTAGAACATCATTTCCAGTTACAGTGTGAATGGAATACTTC
ENV GENOMIC HERV-KII (1309) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATTGTTTCCAGTTACAGTGTGACTGGAATACGTC
ENV GENOMIC AC008813 (1238) ----------
ENV GENOMIC AC012309 (1606) AGAC----TGTCATTTGGATGGGAGATAGGCTCATGAGCTTAGAACATCATTTCCAGTTACAGTGTGACTGGAATACGTC
ENV GENOMIC AL121932 (1538) ----------
ENV GENOMIC AD000090 (1616) AGACAAACTGTCATTTGGATGGGAGACAGGCTCATGAGCTTAGAACATCGTTTCCAGTTACAGTGTGACTGGAATACGTC
ENV GEN AL160008 (647) ----------
ENV GENOMIC HEU32496 (441) ----------
ENV GENOMIC AC011467 (1279) AGACAAACTGTCATTTGGGTGGGAGACAGACTCATGAGCTTAGAACATCATTTCCAGTTACGATGTGACTGGAATATCTC
ENV GENOMIC AF235103 (1672) AGACAAACTGTCATTTGGATGGGAGATAGGCTCATAAGTTTGGAATATCTTTTTCAGTTACTGTGTGACTACAATACATC
ENV GENOMIC AC026786 (1548) AGACAAACTGTCATTTGGATGGGAGATAGGCTCATGAGCCTGGAATATCTTTTTCAGTTA--GTGTGACTGGACTACGTC
ENV GENOMIC AC034203 (1403) ----------
ENV GENOMIC AC018809 (1309) AGACAAACTGTCATTTGGATGGGAGACAGGCTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATATGTC
ENV GENOMIC HERV-K102 AF164610 (1365) AGACAAACTGTCATTTGGATGGGAGACAGACTCATGAGCTTAGAACATCGTTTCCAGTTACAATGTGACTGGAATACGTC
ENV GENOMIC FRAG. AF260253 (1) ----------
CONSENSUS (2081) AGACAAACTGTCATTTGGATGGGAGA AG CTCATGAGCTT GAA ATC TTT CAGTTACA TGTGACTGGAATACGTC

FIG. 6-27

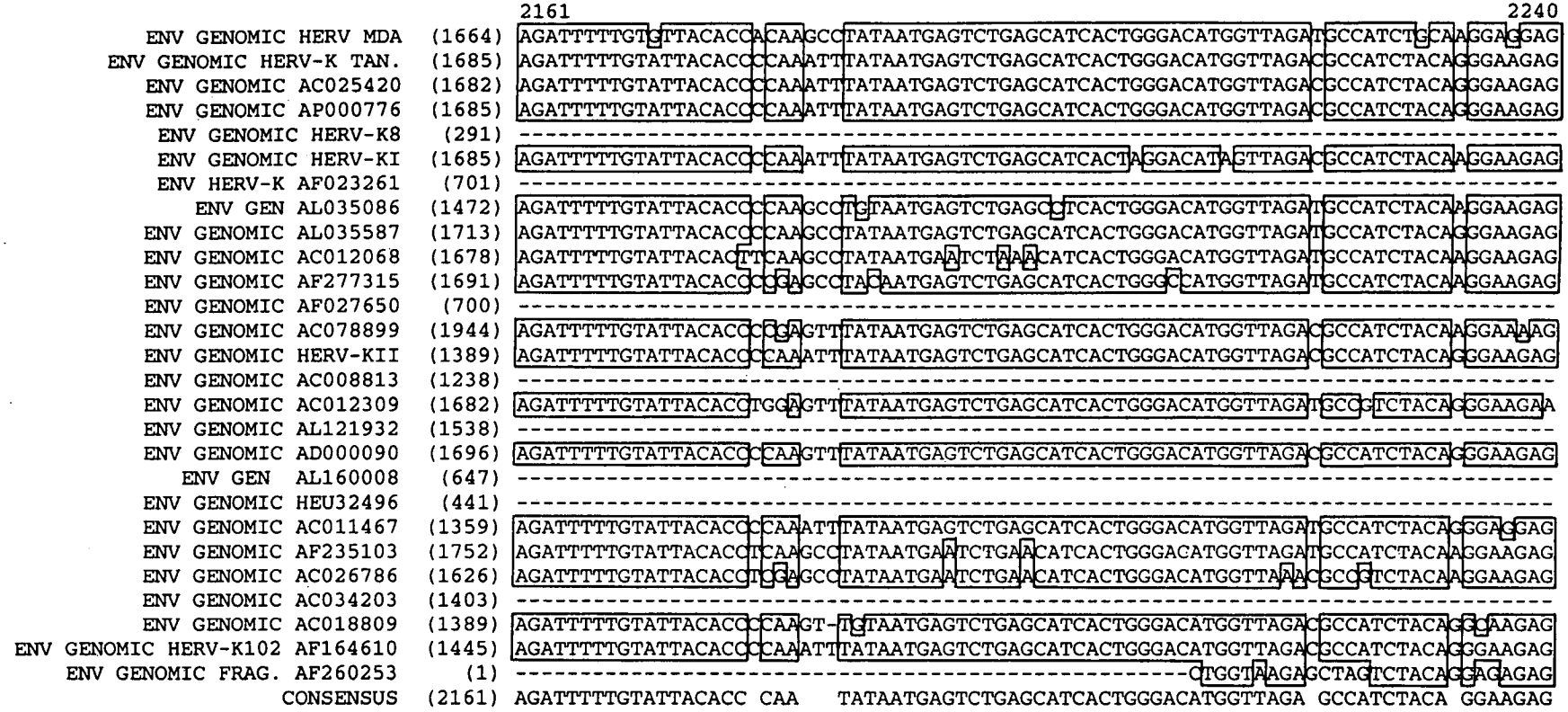
2161
2240
ENV GENOMIC HERV MDA (1664)
ENV GENOMIC HERV-K TAN. (1685)
ENV GENOMIC AC025420 (1682)
ENV GENOMIC AP000776 (1685)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1685)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1472)
ENV GENOMIC AL035587 (1713)
ENV GENOMIC AC012068 (1678)
ENV GENOMIC AF277315 (1691)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (1944)
ENV GENOMIC HERV-KII (1389)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1682)
ENV GENOMIC AL121932 (1538)
ENV GENOMIC AD000090 (1696)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1359)
ENV GENOMIC AF235103 (1752)
ENV GENOMIC AC026786 (1626)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1389)
ENV GENOMIC HERV-K102 AF164610 (1445)
ENV GENOMIC FRAG. AF260253 (1)
CONSENSUS (2161) AGATTTTTGTATTACACC CAA TATAATGAGTCTGAGCATCACTGGGACATGGTTAGA GCCATCTACA GGAAGAG

FIG. 6-28

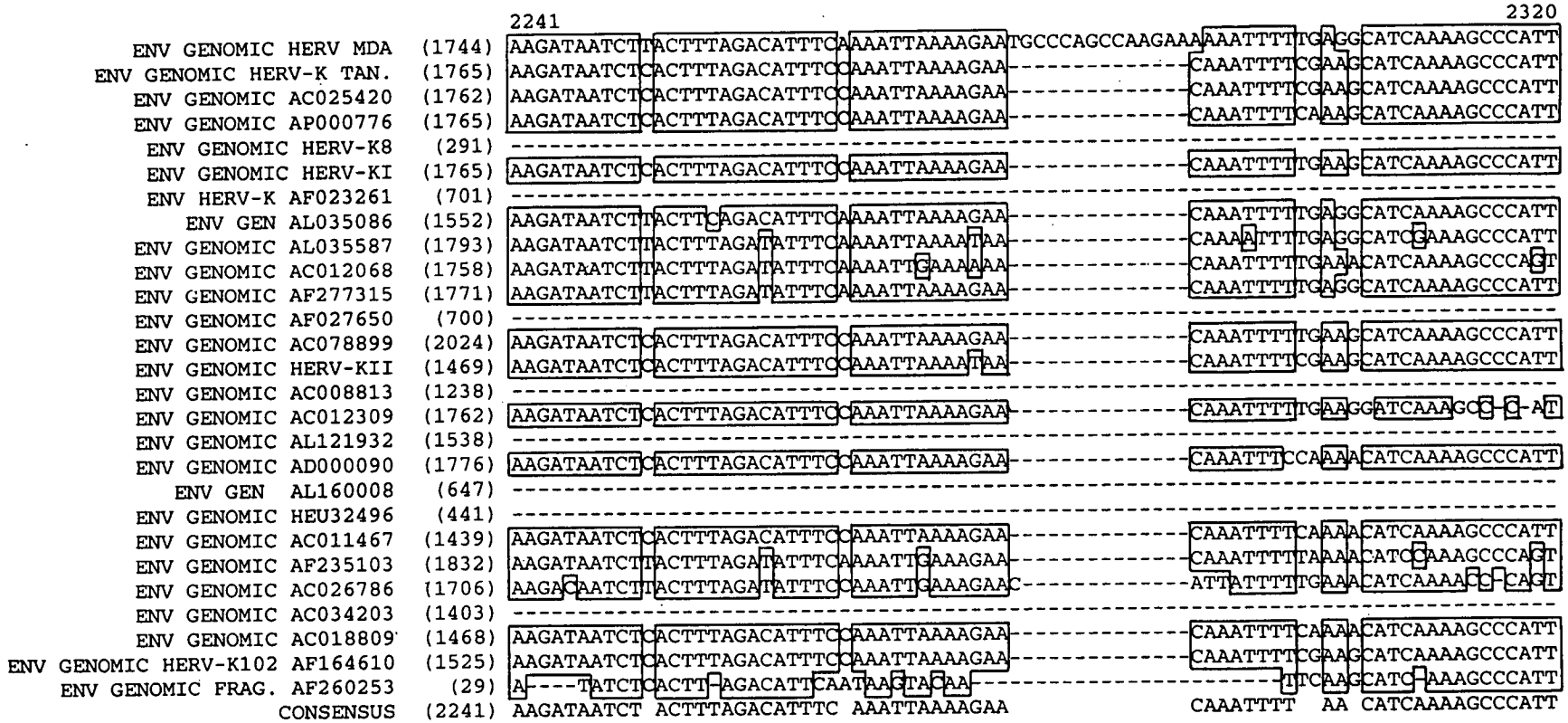
2241
2320
ENV GENOMIC HERV MDA (1744)
ENV GENOMIC HERV-K TAN. (1765)
ENV GENOMIC AC025420 (1762)
ENV GENOMIC AP000776 (1765)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1765)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1552)
ENV GENOMIC AL035587 (1793)
ENV GENOMIC AC012068 (1758)
ENV GENOMIC AF277315 (1771)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (2024)
ENV GENOMIC HERV-KII (1469)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1762)
ENV GENOMIC AL121932 (1538)
ENV GENOMIC AD000090 (1776)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1439)
ENV GENOMIC AF235103 (1832)
ENV GENOMIC AC026786 (1706)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1468)
ENV GENOMIC HERV-K102 AF164610 (1525)
ENV GENOMIC FRAG. AF260253 (29)
CONSENSUS (2241) AAGATAATCT ACTTTAGACATTTC AAATTAAAAGAA CAAATTTT AA CATCAAAAGCCCATT

FIG. 6-29

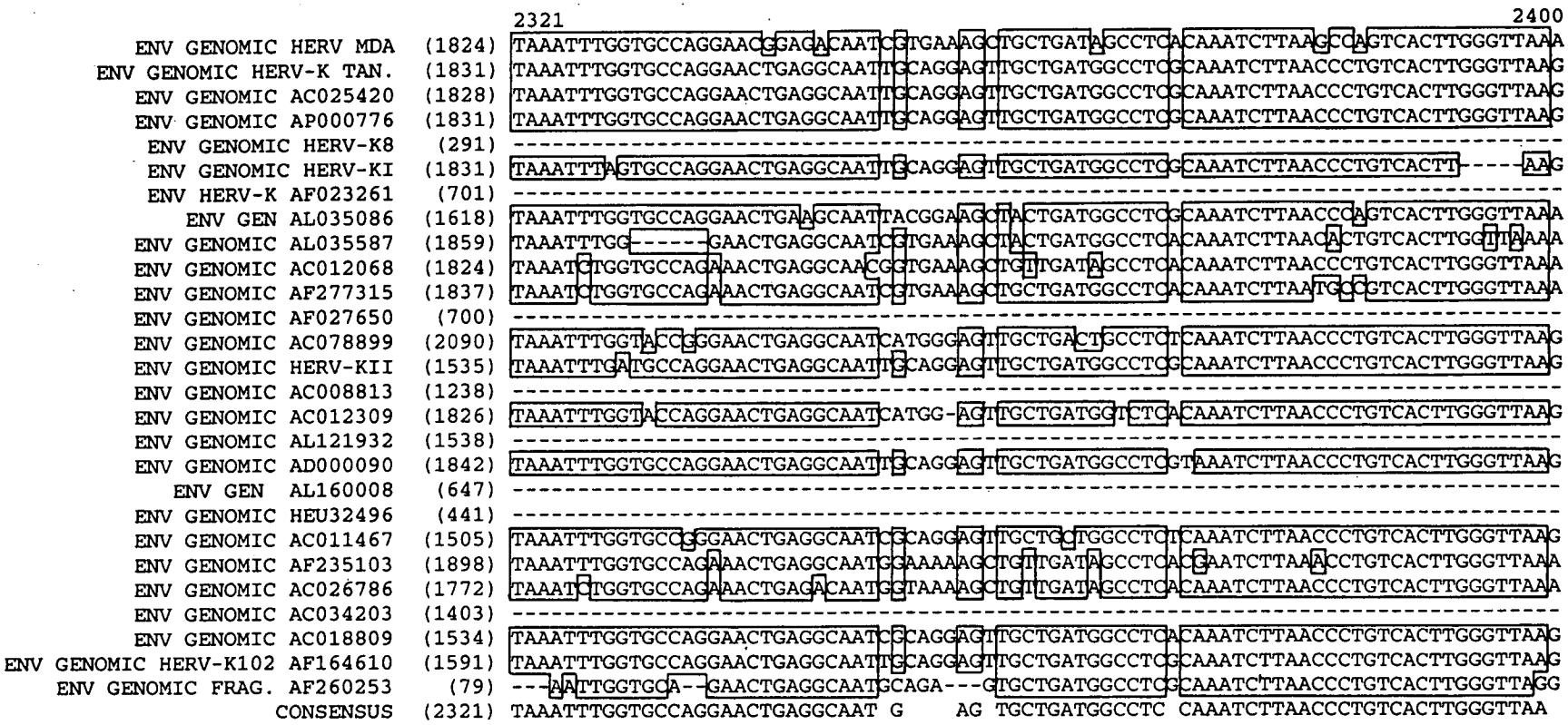
2321
2400
ENV GENOMIC HERV MDA (1824) TAAATTTGGTGCCAGGAACGGAGACAATCGTGAAAGCTGCTGATAGCCTCACAAATCTTAAGCCAGTCACTTGGGTTAAA
ENV GENOMIC HERV-K TAN. (1831) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC AC025420 (1828) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC AP000776 (1831) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC HERV-K8 (291) ----------
ENV GENOMIC HERV-KI (1831) TAAATTTAGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTT----AAG
ENV HERV-K AF023261 (701) ----------
ENV GEN AL035086 (1618) TAAATTTGGTGCCAGGAACTGAAGCAATTACGGAAGCTACTGATGGCCTCGCAAATCTTAACCCAGTCACTTGGGTTAAA
ENV GENOMIC AL035587 (1859) TAAATTTGG-----GAACTGAGGCAATCGTGAAAGCTACTGATGGCCTCACAAATCTTAACACTGTCACTTGGTTAAAA
ENV GENOMIC AC012068 (1824) TAAATCTGGTGCCAGAAACTGAGGCAACGGTGAAAGCTGTTGATAGCCTCACAAATCTTAACCCTGTCACTTGGGTTAAA
ENV GENOMIC AF277315 (1837) TAAATCTGGTGCCAGAAACTGAGGCAATCGTGAAAGCTGCTGATGGCCTCACAAATCTTAATGCCGTCACTTGGGTTAAA
ENV GENOMIC AF027650 (700) ----------
ENV GENOMIC AC078899 (2090) TAAATTTGGTACCGGGAACTGAGGCAATCATGGGAGTTGCTGACTGCCTCTCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC HERV-KII (1535) TAAATTTGATGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC AC008813 (1238) ----------
ENV GENOMIC AC012309 (1826) TAAATTTGGTACCAGGAACTGAGGCAATCATGG-AGTTGCTGATGGTCTCACAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC AL121932 (1538) ----------
ENV GENOMIC AD000090 (1842) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGTAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GEN AL160008 (647) ----------
ENV GENOMIC HEU32496 (441) ----------
ENV GENOMIC AC011467 (1505) TAAATTTGGTGCCGGGAACTGAGGCAATCGCAGGAGTTGCTGGTGGCCTCTCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC AF235103 (1898) TAAATTTGGTGCCAGAAACTGAGGCAATGGAAAAAGCTGTTTGATAGCCTCACGAATCTTAAACCTGTCACTTGGGTTAAA
ENV GENOMIC AC026786 (1772) TAAATCTGGTGCCAGAAACTGAGACAATGGTAAAAGCTGTTGATAGCCTCACAAATCTTAACCCTGTCACTTGGGTTAAA
ENV GENOMIC AC034203 (1403) ----------
ENV GENOMIC AC018809 (1534) TAAATTTGGTGCCAGGAACTGAGGCAATCGCAGGAGTTGCTGATGGCCTCACAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC HERV-K102 AF164610 (1591) TAAATTTGGTGCCAGGAACTGAGGCAATTGCAGGAGTTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAAG
ENV GENOMIC FRAG. AF260253 (79) ---AATTGGTGCA--GAACTGAGGCAATGCAGA---GTGCTGATGGCCTCGCAAATCTTAACCCTGTCACTTGGGTTAGG
CONSENSUS (2321) TAAATTTGGTGCCAGGAACTGAGGCAAT G AG TGCTGATGGCCTC CAAATCTTAACCCTGTCACTTGGGTTAA

FIG. 6-30

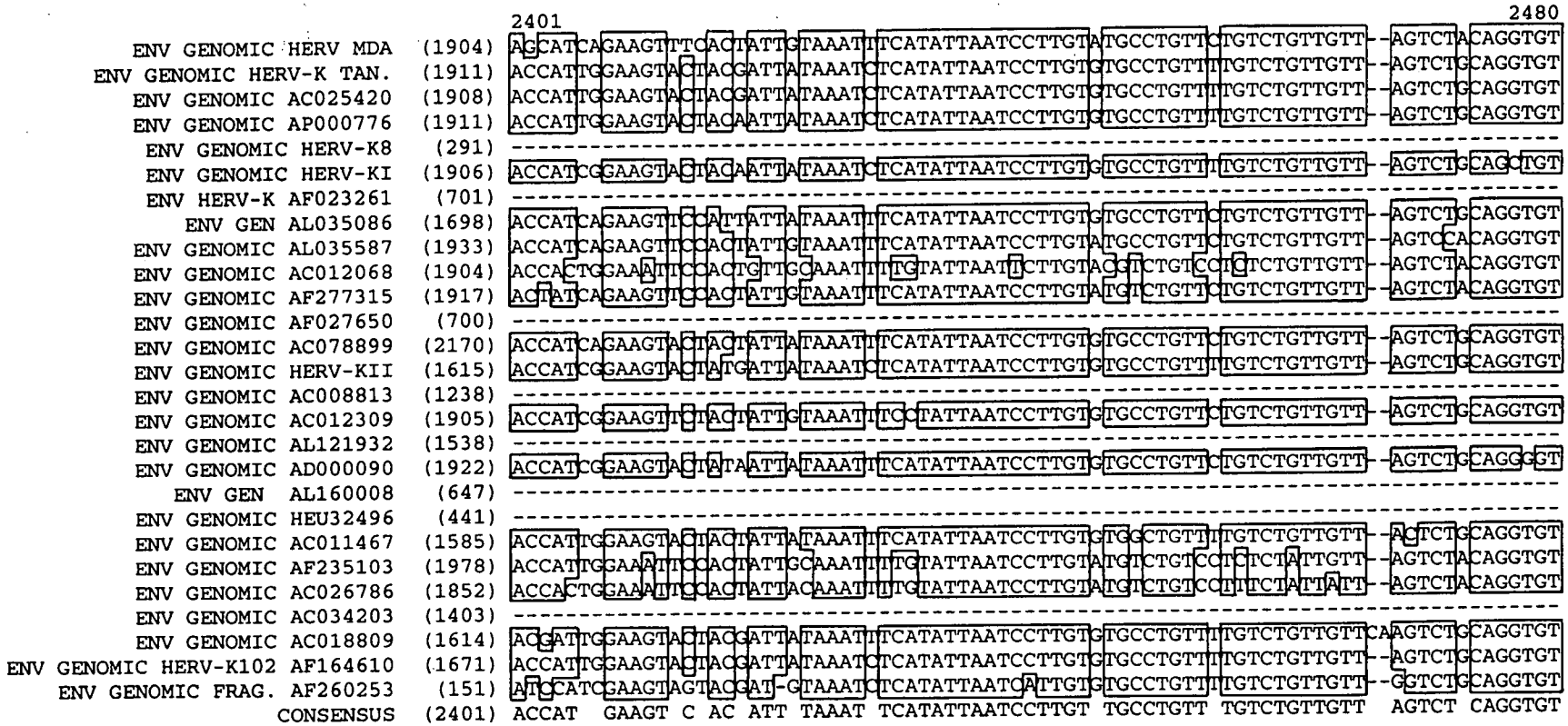
2401
2480
ENV GENOMIC HERV MDA (1904)
ENV GENOMIC HERV-K TAN. (1911)
ENV GENOMIC AC025420 (1908)
ENV GENOMIC AP000776 (1911)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1906)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1698)
ENV GENOMIC AL035587 (1933)
ENV GENOMIC AC012068 (1904)
ENV GENOMIC AF277315 (1917)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (2170)
ENV GENOMIC HERV-KII (1615)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1905)
ENV GENOMIC AL121932 (1538)
ENV GENOMIC AD000090 (1922)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1585)
ENV GENOMIC AF235103 (1978)
ENV GENOMIC AC026786 (1852)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1614)
ENV GENOMIC HERV-K102 AF164610 (1671)
ENV GENOMIC FRAG. AF260253 (151)
CONSENSUS (2401) ACCAT GAAGT C AC ATT TAAAT TCATATTAATCCTTGT TGCCTGTT TGTCTGTTGTT AGTCT CAGGTGT

FIG. 6-31

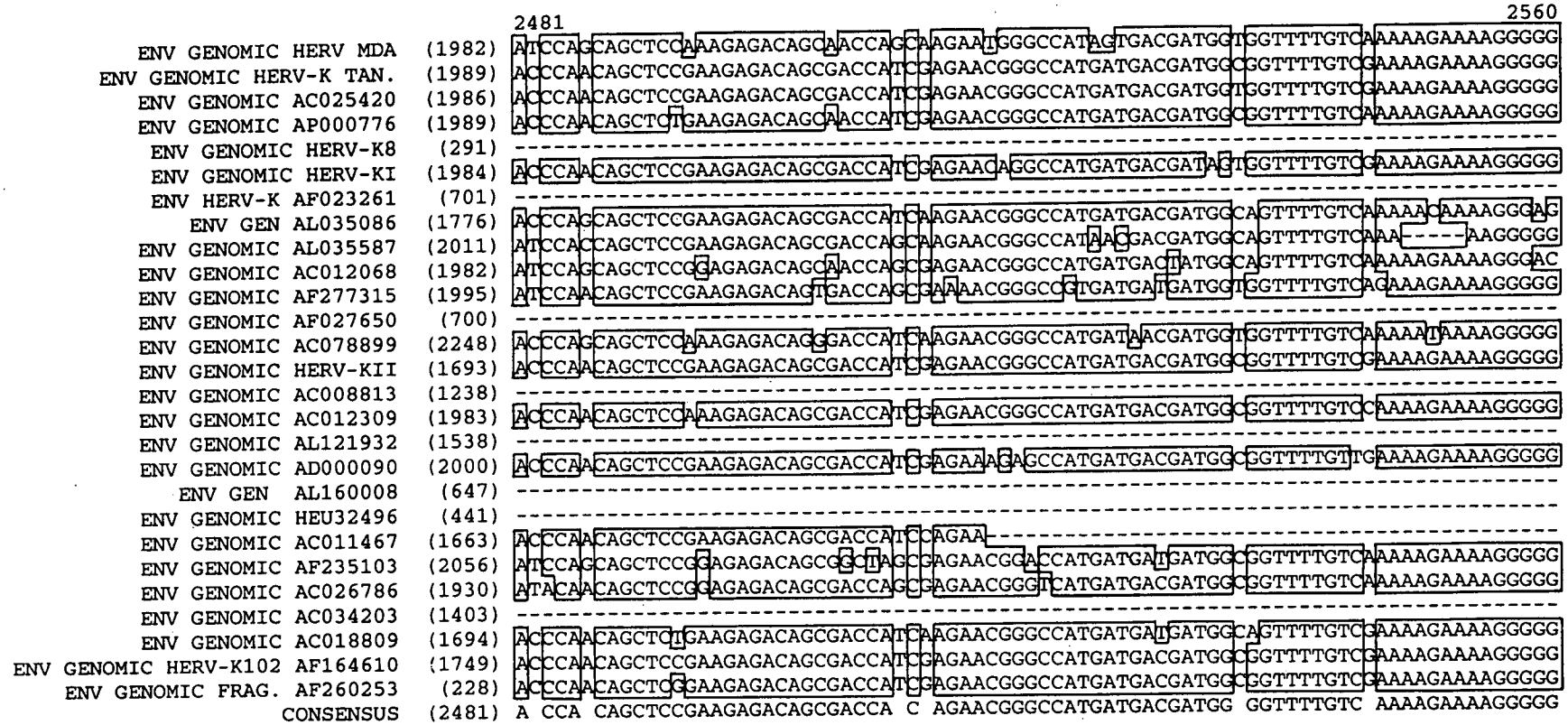
2481
2560
ENV GENOMIC HERV MDA (1982)
ENV GENOMIC HERV-K TAN. (1989)
ENV GENOMIC AC025420 (1986)
ENV GENOMIC AP000776 (1989)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (1984)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1776)
ENV GENOMIC AL035587 (2011)
ENV GENOMIC AC012068 (1982)
ENV GENOMIC AF277315 (1995)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (2248)
ENV GENOMIC HERV-KII (1693)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (1983)
ENV GENOMIC AL121932 (1538)
ENV GENOMIC AD000090 (2000)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1663)
ENV GENOMIC AF235103 (2056)
ENV GENOMIC AC026786 (1930)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1694)
ENV GENOMIC HERV-K102 AF164610 (1749)
ENV GENOMIC FRAG. AF260253 (228)
CONSENSUS (2481) A CCA CAGCTCCGAAGAGACAGCGACCA C AGAACGGGCCATGATGACGATGG GGTTTTGTC AAAAGAAAAGGGGG

FIG. 6-32

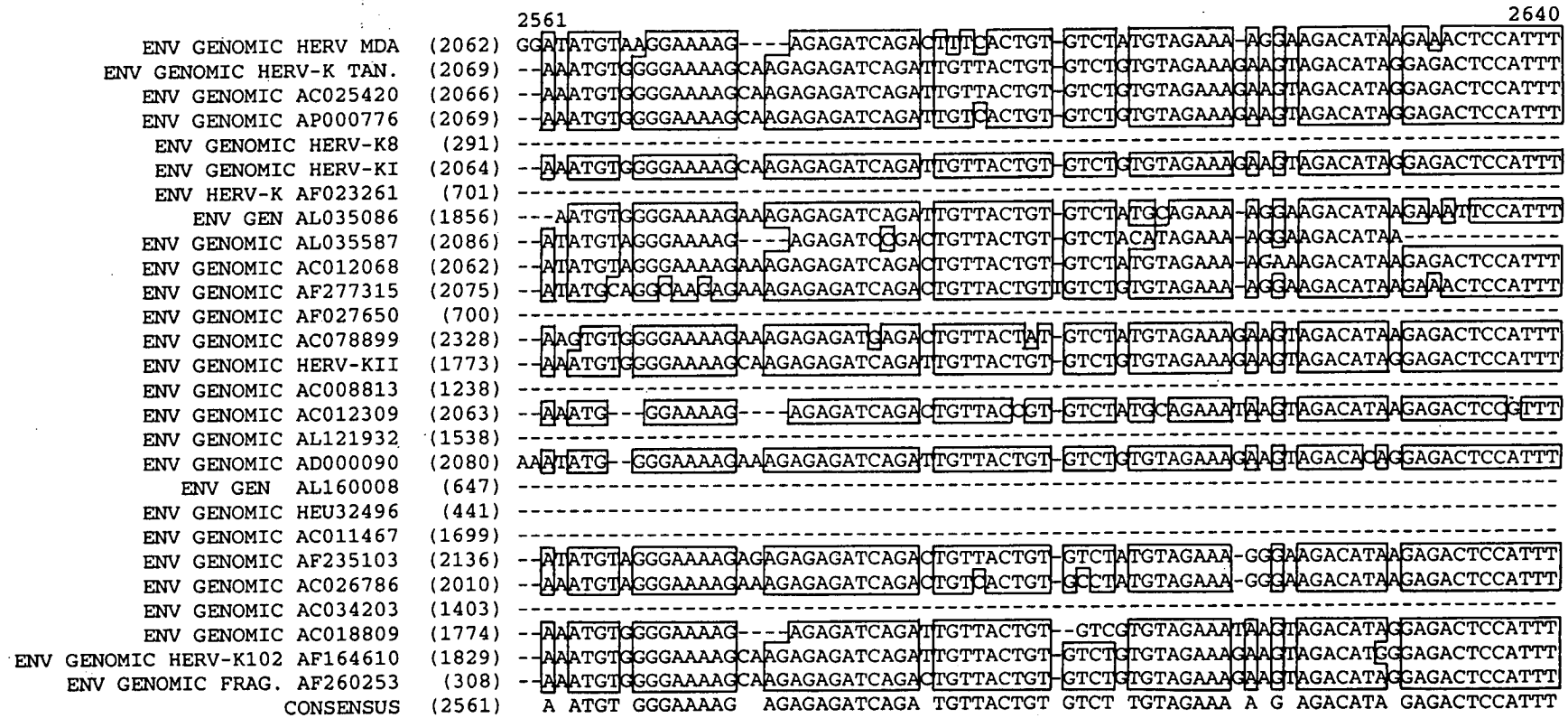
2561
2640
ENV GENOMIC HERV MDA (2062)
ENV GENOMIC HERV-K TAN. (2069)
ENV GENOMIC AC025420 (2066)
ENV GENOMIC AP000776 (2069)
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (2064)
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1856)
ENV GENOMIC AL035587 (2086)
ENV GENOMIC AC012068 (2062)
ENV GENOMIC AF277315 (2075)
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (2328)
ENV GENOMIC HERV-KII (1773)
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (2063)
ENV GENOMIC AL121932 (1538)
ENV GENOMIC AD000090 (2080)
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1699)
ENV GENOMIC AF235103 (2136)
ENV GENOMIC AC026786 (2010)
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1774)
ENV GENOMIC HERV-K102 AF164610 (1829)
ENV GENOMIC FRAG. AF260253 (308)
CONSENSUS (2561) A ATGT GGGAAAAG AGAGAGATCAGA TGTTACTGT GTCT TGTAGAAA A G AGACATA GAGACTCCATTT

FIG. 6-33

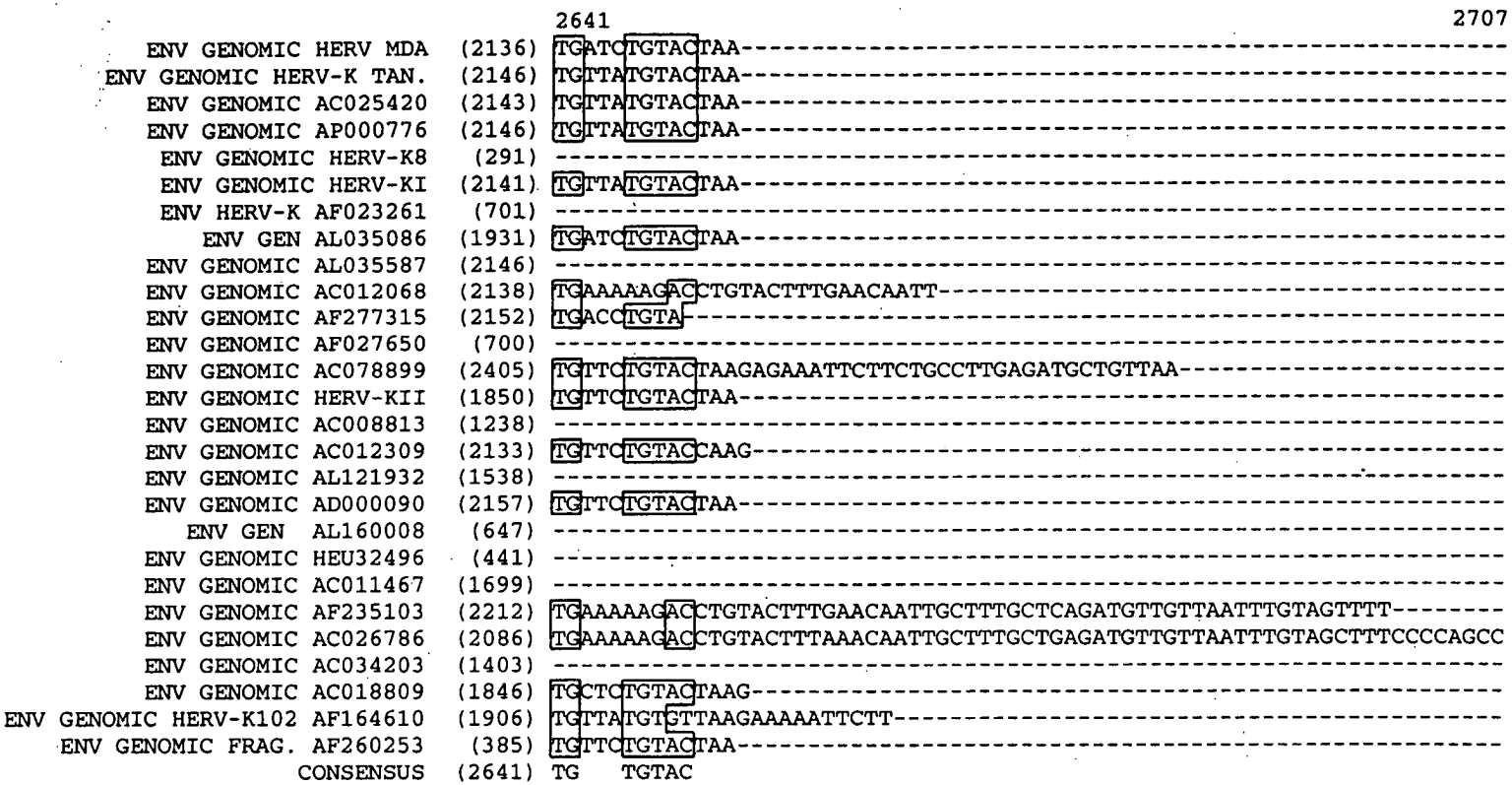
2641
2707
ENV GENOMIC HERV MDA (2136) TGATCTGTACTAA
ENV GENOMIC HERV-K TAN. (2146) TGTTATGTACTAA
ENV GENOMIC AC025420 (2143) TGTTATGTACTAA
ENV GENOMIC AP000776 (2146) TGTTATGTACTAA
ENV GENOMIC HERV-K8 (291)
ENV GENOMIC HERV-KI (2141) TGTTATGTACTAA
ENV HERV-K AF023261 (701)
ENV GEN AL035086 (1931) TGATCTGTACTAA
ENV GENOMIC AL035587 (2146)
ENV GENOMIC AC012068 (2138) TGAAAAAGACCTGTACTTTGAACAATT
ENV GENOMIC AF277315 (2152) TGACCTGTA
ENV GENOMIC AF027650 (700)
ENV GENOMIC AC078899 (2405) TGTTCTGTACTAAGAGAAATTCTTCTGCCTTGAGATGCTGTTAA
ENV GENOMIC HERV-KII (1850) TGTTCTGTACTAA
ENV GENOMIC AC008813 (1238)
ENV GENOMIC AC012309 (2133) TGTTCTGTACCAAG
ENV GENOMIC AL121932 (1538)
ENV GENOMIC AD000090 (2157) TGTTCTGTACTAA
ENV GEN AL160008 (647)
ENV GENOMIC HEU32496 (441)
ENV GENOMIC AC011467 (1699)
ENV GENOMIC AF235103 (2212) TGAAAAAGACCTGTACTTTGAACAATTGCTTTGCTCAGATGTTGTTAATTTGTAGTTTT
ENV GENOMIC AC026786 (2086) TGAAAAAGACCTGTACTTTAAACAATTGCTTTGCTGAGATGTTGTTAATTTGTAGCTTTCCCCAGCC
ENV GENOMIC AC034203 (1403)
ENV GENOMIC AC018809 (1846) TGCTCTGTACTAAG
ENV GENOMIC HERV-K102 AF164610 (1906) TGTTATGTGTTAAGAAAAATTCTT
ENV GENOMIC FRAG. AF260253 (385) TGTTCTGTACTAA
CONSENSUS (2641) TG TGTAC

FIG. 6-34

```
                                    1                                                          60
GI_4185938_EMB_CAA76878.1_     (1) -----MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTL
GI_4185942_EMB_CAA76881.1_     (1) -----MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTL
GI_4185946_EMB_CAA76884.1_     (1) -----MGQTKSKIKSKYASYLSFIKILLKRGGVKVSTKNLIKLFQIIEQFCPWFPEQGTL
GI_5931704_EMB_CAB56602.1_     (1) -------MGQTKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQTTEQFCPWFPEQGNL
           GAG OF AB047240     (1) -----MGQTKSKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQIIEQFCPWFPEQGTL
      TRANSLATION OF ORF99     (1) YKKAGLGQTKSKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQIIEQFCPWFPEQGTL
TRANSLATION OF G226TOP-LINK    (1) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG    (1) -----MGQTKSKTKSKYASYLSFIKILLKRGGVRVSTKNLIKLFQIIEQFCPWFPEQGTL
                GAG106-135     (1) ------------------------------------------------------------
                GAG186-215     (1) ------------------------------------------------------------
                  GAG46-75     (1) ----------------------------------------------CPWFPEQGTL
                    PDG-G1     (1) ------------------------------------------------------------
                    PGD-G2     (1) ------------------------------------------------------------
                    PGD-G3     (1) ------------------------------------------------------------
                 CONSENSUS     (1)                                                CPWFPEQG L

                                    61                                                         120
GI_4185938_EMB_CAA76878.1_    (56) DLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTEEDSVSVSDAPGSCIIDC
GI_4185942_EMB_CAA76881.1_    (56) DLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTEEDSVSVSDAPGSCIIDC
GI_4185946_EMB_CAA76884.1_    (56) DLKDWKRIGKELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTEEDSVSVSDAPGSCIIDC
GI_5931704_EMB_CAB56602.1_    (54) DLEDWKRIGKELKQAGRKGNIIPLTVWNDWPIIKAALEPFQTEDS-VSVSDAPGSCIIDC
           GAG OF AB047240    (56) DLKDWKRIGEELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTKEDSVSVSDAPGSCVIDC
      TRANSLATION OF ORF99    (61) DLKDWKRIGEELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTKEDSVSVSDAPGSCVIDC
TRANSLATION OF G226TOP-LINK   (1) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG   (56) DLKDWKRIGEELKQAGRKGNIIPLTVWNDWAIIKAALEPFQTKEDSVSVSDAPGSCVIDC
                GAG106-135    (1) ----------------------------------------------DAPGSCIIDC
                GAG186-215    (1) ------------------------------------------------------------
                  GAG46-75    (11) DLKDWKRIGKELKQAGRKGN----------------------------------------
                    PDG-G1    (1) ---DWKRIGKELKQAGRKG------------------------------------------
                    PGD-G2    (1) ------------------------------------------------------------
                    PGD-G3    (1) ------------------------------------------------------------
                 CONSENSUS    (61) DL DWKRIG ELKQAGRKGN                                DAPGSCIIDC
```

FIG. 7-1

```
                                        121                                                                 180
GI_4185938_EMB_CAA76878.1_   (116) NENTRKKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSE
GI_4185942_EMB_CAA76881.1_   (116) NENTRKKKSQKETESLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSE
GI_4185946_EMB_CAA76884.1_   (116) NENTRKKKSQKETEGLHCEYVAEPVMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPSE
GI_5931704_EMB_CAB56602.1_   (113) NEKTRKKKSQKETETLHCEYVAEPLMAQSTQNVDYNQLQEVIYPETLKLEGKGPELVGPLE
            GAG OF AB047240  (116) NEKTGRKKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIYPETLKLEGKGPELVGPSE
       TRANSLATION OF ORF99  (121) NEKTGRKKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIYPETLKLEGKGPELVGPSE
TRANSLATION OF G226TOP-LINK   (1) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG  (116) NEKTGRKKSQKETESLHCEYVTEPVMAQSTQNVDYNQLQGVIYPETLKLEGKGPELVGPSE
                GAG106-135   (11) NENTRKKKSQKETEGLHCEYV----------------------------------------
                GAG186-215    (1) ------------------------------------------------------------
                  GAG46-75   (31) ------------------------------------------------------------
                     PDG-G1  (17) ------------------------------------------------------------
                     PGD-G2   (1) ------------------------------------------------------------
                     PGD-G3   (1) ------------------------------------------------------------
                  CONSENSUS (121) NE T KKSQKETE LHCEYV

                                        181                                                                 240
GI_4185938_EMB_CAA76878.1_   (176) SKPRGTSPLPAGQVPVTLQPQKQVKENKTQPPVAYQYWPPAELQYRPPPESQYGYPGMPP
GI_4185942_EMB_CAA76881.1_   (176) SKPRGTSRLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYRPPVESQYGYPGMPP
GI_4185946_EMB_CAA76884.1_   (176) SKPRGTSPLPAGQVPVTLQPQKQVKENKTQPPVAYQYWPPAELQYRPPPESQYGYPGMPP
GI_5931704_EMB_CAB56602.1_   (173) SKPRGPSPLSAGQVTVTLQPQAQVRENKTQLPVAYQYWPPAELQYRPPPESQYGYLGMPP
            GAG OF AB047240  (176) SKPRGPSPLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYLPPPESQYGYPGMPP
       TRANSLATION OF ORF99  (181) SKPRGPSPLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYLPPPESQYGYPGMPP
TRANSLATION OF G226TOP-LINK   (1) ----------------------------------------------------SQYGYPGMPP
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG  (176) SKPRGPSPLPAGQVPVTLQPQTQVKENKTQPPVAYQYWPPAELQYLPPPESQYGYPGMPP
                GAG106-135   (31) ------------------------------------------------------------
                GAG186-215    (1) ----------AGQVPVTLQPQKQVKENKTQPPVAYQYWPP--------------------
                  GAG46-75   (31) ------------------------------------------------------------
                     PDG-G1  (17) ------------------------------------------------------------
                     PGD-G2   (1) ------------------------------------------------------------
                     PGD-G3   (1) ------------------------------------------------------------
                  CONSENSUS (181)           AGQV VTLQPQ QVKENKTQ PVAYQYWPP          SQYGY GMPP
```

FIG. 7-2

```
                                        241                                                                  300
GI_4185938_EMB_CAA76878.1_   (236) APQGRAPYPQPPTRRLNPTAPPSRQGSKLHEIIDKSRKEGDTEAWQFPVTLEPMPPGEGA
GI_4185942_EMB_CAA76881.1_   (236) APQGRAPYPQPPTRRLNPTAPPSRRGSELHEIIDKSRKEGDTEAWQFPVMLEPMPPGEGA
GI_4185946_EMB_CAA76884.1_   (236) APQGRAPYPQPPTRRLNPTAPPSRQGSKLHEIIDKSRKEGDTEAWQFPVTLEPMPPGEGA
GI_5931704_EMB_CAB56602.1_   (233) APQDREPYPQPPTRRQCYGTT-------------------------------------------
                GAG OF AB047240 (236) ALQGRAPYPQPPTVRLNPTASRSGQGGTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET
              TRANSLATION OF ORF99 (241) ALQGRAPYPQPPTVRLNPTASRSGQGGTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET
TRANSLATION OF G226TOP-LINK  (11) APQGRAPYPQPPTRRLNPTA-------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) -----------------------------------------------------------------
           TRANSLATION OF LNCAP-GAG (236) ALQGRAPYPQPPTVRLNPTASRSGQGGTLHAVIDEARKQGDLEAWRFLVILQLVQAGEET
                        GAG106-135  (31) -----------------------------------------------------------------
                        GAG186-215  (31) -----------------------------------------------------------------
                          GAG46-75  (31) -----------------------------------------------------------------
                             PDG-G1 (17) -----------------------------------------------------------------
                             PGD-G2  (1) --------------------------SKLHEIIDKSRKEGDT------------------
                             PGD-G3  (1) -----------------------------------------------------------------
                          CONSENSUS (241) A Q R PYPQPPT R


                                        301                                                                  360
GI_4185938_EMB_CAA76878.1_   (296) QEGEPPTVEARYKSFSIKKLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAK
GI_4185942_EMB_CAA76881.1_   (296) QEGEPPTVEARYKSFSIKMLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAK
GI_4185946_EMB_CAA76884.1_   (296) QEGEPPTVEARYKSFSIKKLKDMKEGVKQYGPNSPYMRTLLDSIAHGHRLIPYDWEILAK
GI_5931704_EMB_CAB56602.1_   (254) -----------------------------------------------------------------
                GAG OF AB047240 (296) QVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIAHGNRLTPYDWESLAK
              TRANSLATION OF ORF99 (301) QVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIAHGNRLTPYDWESLAK
TRANSLATION OF G226TOP-LINK  (31) -----------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) -----------------------------------------------------------------
           TRANSLATION OF LNCAP-GAG (296) QVGAPARAETRCEPFTMKMLKDIKEGVKQYGSNSPYIRTLLDSIAHGNRLTPYDWESLAK
                        GAG106-135  (31) -----------------------------------------------------------------
                        GAG186-215  (31) -----------------------------------------------------------------
                          GAG46-75  (31) -----------------------------------------------------------------
                             PDG-G1 (17) -----------------------------------------------------------------
                             PGD-G2 (17) -----------------------------------------------------------------
                             PGD-G3  (1) -----------------------------------------------------------------
                          CONSENSUS (301)
```

FIG. 7-3

```
                                          361                                                                 420
GI_4185938_EMB_CAA76878.1_  (356) SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA
GI_4185942_EMB_CAA76881.1_  (356) SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA
GI_4185946_EMB_CAA76884.1_  (356) SSLSPSQFLQFKTWWIDGVQEQVRRNRAANPPVNIDADQLLGIGQNWSTISQQALMQNEA
GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
           GAG OF AB047240  (356) SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
      TRANSLATION OF ORF99  (361) SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
TRANSLATION OF G226TOP-LINK  (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG  (356) SSLSSSQYLQFKTWWIDGVQEQVRKNQATKPTVNIDADQLLGTGPNWSTINQQSVMQNEA
               GAG106-135    (31) ------------------------------------------------------------
               GAG186-215    (31) ------------------------------------------------------------
                 GAG46-75    (31) ------------------------------------------------------------
                    PDG-G1   (17) ------------------------------------------------------------
                    PGD-G2   (17) ------------------------------------------------------------
                    PGD-G3    (1) ------------------------------------------------------------
                 CONSENSUS  (361)

                                          421                                                                 480
GI_4185938_EMB_CAA76878.1_  (416) IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI
GI_4185942_EMB_CAA76881.1_  (416) IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIANEKARKVI
GI_4185946_EMB_CAA76884.1_  (416) IEQVRAICLRAWEKIQDPGSTCPSFNTVRQGSKEPYPDFVARLQDVAQKSIADEKARKVI
GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
           GAG OF AB047240  (416) IEQVRAICLRAWGKIQDPGTAFP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
      TRANSLATION OF ORF99  (421) IEQVRAICLRAWGKIQDPGTAF-PINSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
TRANSLATION OF G226TOP-LINK  (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK   (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG  (416) IEQVRAICLRAWGKIQDPGTAFP-INSIRQGSKEPYPDFVARLQDAAQKSITDDNARKVI
               GAG106-135    (31) ------------------------------------------------------------
               GAG186-215    (31) ------------------------------------------------------------
                 GAG46-75    (31) ------------------------------------------------------------
                    PDG-G1   (17) ------------------------------------------------------------
                    PGD-G2   (17) ------------------------------------------------------------
                    PGD-G3    (1) ------------------------------------------------------------
                 CONSENSUS  (421)
```

FIG. 7-4

```
                                        481                                                                 540
GI_4185938_EMB_CAA76878.1_  (476) VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMYKAMLMAQAITGVVL
GI_4185942_EMB_CAA76881.1_  (476) VELMAYENPNPECQSAIKPLKGKVPAGSDVISEYVKACDGMGGAMHKAMLMAQAITGVVL
GI_4185946_EMB_CAA76884.1_  (476) VELMAYENANPECQSAIKPLKGKVPAGSDVISEYVKACDGIGGAMHKAMLMAQAITGVVL
GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
             GAG OF AB047240  (475) VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
       TRANSLATION OF ORF99   (480) VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
TRANSLATION OF G226TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK    (1) ------------------------------------------------------------
   TRANSLATION OF LNCAP-GAG   (475) VELMAYENANPECQSAIKPLKGKVPAGVDVITEYVKACDGIGGAMHKAMLMAQAMRGLTL
                GAG106-135    (31) ------------------------------------------------------------
                GAG186-215    (31) ------------------------------------------------------------
                  GAG46-75    (31) ------------------------------------------------------------
                     PDG-G1   (17) ------------------------------------------------------------
                     PGD-G2   (17) ------------------------------------------------------------
                     PGD-G3    (1) ------------------------------------------------------------
                  CONSENSUS  (481)

                                        541                                                                 600
GI_4185938_EMB_CAA76878.1_  (536) GGQVRTFGRKCYNCGQIGHLKKNCPVLNKQNITIQATTTG-REPPDLCPRCKKGKHWASQ
GI_4185942_EMB_CAA76881.1_  (536) GGQVRTFGGKCYNCGQIGHLKKNCPVLNKQNITIQATTTG-REPPDLCPRCKKGKHWASQ
GI_4185946_EMB_CAA76884.1_  (536) GGQVRTFGRKCYNCGQIGHLKKNCPVLNKQNITIQATTTG-REPPDLCPRCKKGKHWASQ
GI_5931704_EMB_CAB56602.1_  (254) ------------------------------------------------------------
             GAG OF AB047240  (535) GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQ
       TRANSLATION OF ORF99   (540) GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQ
TRANSLATION OF G226TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK    (1) ----------------------------------------------------------WASQ
   TRANSLATION OF LNCAP-GAG   (535) GGQVRTFGKKCYNCGQIGHLKRSCPVLNKQNIINQAITAKNKKPSGLCPKCGKGKHWANQ
                GAG106-135    (31) ------------------------------------------------------------
                GAG186-215    (31) ------------------------------------------------------------
                  GAG46-75    (31) ------------------------------------------------------------
                     PDG-G1   (17) ------------------------------------------------------------
                     PGD-G2   (17) ------------------------------------------------------------
                     PGD-G3    (1) ------------------------------------------------------------
                  CONSENSUS  (541)
```

FIG. 7-5

```
                                        601                                                                 660
GI_4185938_EMB_CAA76878.1_   (595) CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ
GI_4185942_EMB_CAA76881.1_   (595) CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFPIQPFVPHGFQGQQP-PLSQVFQGISQLPQ
GI_4185946_EMB_CAA76884.1_   (595) CRSKFDKNGQPLSGNEQRGQPQAPQQTGAFPIQPFVPQGFQGQQP-PLSQVFQGISQLPQ
GI_5931704_EMB_CAB56602.1_   (254) ------------------------------------------------------------
           GAG OF AB047240   (595) CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVPQGFQGQQPLQKIPPLQGVSQLQQ
      TRANSLATION OF ORF99   (600) CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVPQGFQGQQPLQKIPPLQGVSQLQQ
TRANSLATION OF G226TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF G591TOP-LINK    (5) CRSKFDKNGQPLSGNEQRGQPQAPQQ----------------------------------
   TRANSLATION OF LNCAP-GAG  (595) CHSKFDKDGQPLSGNRKRGQPQAPQQTGAFPVQLFVPQGFQGQQPLQKIPPLQGVSQLQQ
                GAG106-135   (31) ------------------------------------------------------------
                GAG186-215   (31) ------------------------------------------------------------
                  GAG46-75   (31) ------------------------------------------------------------
                     PDG-G1  (17) ------------------------------------------------------------
                     PGD-G2  (17) ------------------------------------------------------------
                     PGD-G3   (1) CRSKFDKNGQPLSGNE------------------------------------------------
                  CONSENSUS (601) C SKFDK GQPLSGN


                                        661       673
GI_4185938_EMB_CAA76878.1_   (654) YNNCPPPQAAVQQ
GI_4185942_EMB_CAA76881.1_   (654) YNNCPPPQAAVQQ
GI_4185946_EMB_CAA76884.1_   (654) YNNCPPPQAAVQQ
GI_5931704_EMB_CAB56602.1_   (254) -------------
           GAG OF AB047240   (655) SNSCPAPQQAAPQ
      TRANSLATION OF ORF99   (660) SNSCPAPQQAAPQ
TRANSLATION OF G226TOP-LINK   (31) -------------
TRANSLATION OF G591TOP-LINK   (31) -------------
   TRANSLATION OF LNCAP-GAG  (655) SNSCPAPQQAAPQ
                GAG106-135   (31) -------------
                GAG186-215   (31) -------------
                  GAG46-75   (31) -------------
                     PDG-G1  (17) -------------
                     PGD-G2  (17) -------------
                     PGD-G3  (17) -------------
                  CONSENSUS (661)
```

FIG. 7-6

```
                                          1                                                          60
GI_4185939_EMB_CAA76879.1_      (1) MLTDLRAVN---AVIQPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
GI_4185943_EMB_CAA76882.1_      (1) MLTDLRAVNAVNAVIQPMGPLQPGLPSLAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
GI_4185947_EMB_CAA76885.1_      (1) MLTDLRAVN---AVIQPMGPLQPGLPSPAMIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
GI_5931705_EMB_CAB56603.1_      (1) ----------------------------MIPKDWPLIIIDLKDCFFTIPLAEQDCEKFA
                 ENV OF AB047240 (1) ------------------------------------------------------------
       TRANSLATION OF P386TOP-LINK (1) ------------------------------------------------------------
        TRANSLATION OF POL349-LINK (1) ------------------------------------------------------------
              LNCAP-GENOMEA-POLORF (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA (1) ------------------------------------------------------------
          TRANSLATION OF ORF111-10 (1) ------------------------------------------------------------
                           PGD-P1 (1) ------------------------------------------------------------
                           PGD-P2 (1) ------------------------------------------------------------
                            PGDP3 (1) ------------------------------------------------------------
                        CONSENSUS (1)

                                          61                                                         120
GI_4185939_EMB_CAA76879.1_     (58) FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC
GI_4185943_EMB_CAA76882.1_     (61) FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHYIDDILC
GI_4185947_EMB_CAA76885.1_     (58) FTIPAINNKEPATRFQWKVLPQGMLNSPTICQTFVGRALQPVREKFSDCYIIHCIDDILC
GI_5931705_EMB_CAB56603.1_     (32) FTIPAINNKEPATRFQWKVLPQGMLNSPTLCQTFVGRALQPVRDKFSDCYIIHYFDDILC
                 ENV OF AB047240 (1) ------------------------------------------------------------
       TRANSLATION OF P386TOP-LINK (1) ------------------------------------------------------------
        TRANSLATION OF POL349-LINK (1) ------------------------------------------------------------
              LNCAP-GENOMEA-POLORF (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA (1) ------------------------------------------------------------
          TRANSLATION OF ORF111-10 (1) ------------------------------------------------------------
                           PGD-P1 (1) ------------------------------------------------------------
                           PGD-P2 (1) ------------------------------------------------------------
                            PGDP3 (1) ------------------------------------------------------------
                        CONSENSUS (61)
```

FIG. 8-1

```
                                          121                                                                 180
GI_4185939_EMB_CAA76879.1_   (118) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDT
GI_4185943_EMB_CAA76882.1_   (121) AAEMKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLEMQIENRKIKPPKIEIRKDT
GI_4185947_EMB_CAA76885.1_   (118) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDT
GI_5931705_EMB_CAB56603.1_    (92) AAETKDKLIDCYTFLQAEVANAGLAIASDKIQTSTPFHYLGMQIENRKIKPQKIEIRKDT
                ENV OF AB047240     (1) ------------------------------------------------------------
      TRANSLATION OF P386TOP-LINK   (1) ------------------------------------------------------------
       TRANSLATION OF POL349-LINK   (1) ------------------------------------------------------------
             LNCAP-GENOMEA-POLORF   (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA (1) ------------------------------------------------------------
         TRANSLATION OF ORF111-10   (1) ------------------------------------------------------------
                         PGD-P1     (1) ------------------------------------------IENRKIKPQKIEIRKD-
                         PGD-P2     (1) ------------------------------------------------------------
                          PGDP3     (1) ------------------------------------------------------------
                      CONSENSUS    (121)

                                          181                                                                 240
GI_4185939_EMB_CAA76879.1_   (178) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
GI_4185943_EMB_CAA76882.1_   (181) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
GI_4185947_EMB_CAA76885.1_   (178) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
GI_5931705_EMB_CAB56603.1_   (152) LKTLNDFQKLLGDINWIRPTLGIPTYAMSNLFSILRGDSDLNSKRMLTPEATKEIKLVEE
                ENV OF AB047240     (1) ------------------------------------------------------------
      TRANSLATION OF P386TOP-LINK   (1) ------------------------------------------------------------
       TRANSLATION OF POL349-LINK   (1) ------------------------------------------------------------
             LNCAP-GENOMEA-POLORF   (1) ------------------------------------------------------------
TRANSLATION OF LNCAP-POL-GENA-GOODA (1) ------------------------------------------------------------
         TRANSLATION OF ORF111-10   (1) ------------------------------------------------------------
                         PGD-P1    (17) ------------------------------------------------------------
                         PGD-P2     (1) ------------------------------------------------------------
                          PGDP3     (1) ------------------------------------------------------------
                      CONSENSUS    (181)
```

FIG. 8-2

```
                                          241                                                                  300
GI_4185939_EMB_CAA76879.1_          (238) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIAT
GI_4185943_EMB_CAA76882.1_          (241) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQMAT
GI_4185947_EMB_CAA76885.1_          (238) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIAT
GI_5931705_EMB_CAB56603.1_          (212) KIQSAQINRIDPLAPLQLLIFATAHSPTGIIIQNTDLVEWSFLPHSTVKTFTLYLDQIAT
                  ENV OF AB047240     (1) ------------------------------------------------------------MAT
         TRANSLATION OF P386TOP-LINK  (1) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK  (1) ------------------------------------------------------------
                LNCAP-GENOMEA-POLORF  (1) ----------DHLAPLQLLIFGTAHSLTAIIVQNTDLVDWSFLPHSTIKTFTLYLDQMAT
TRANSLATION OF LNCAP-POL-GENA-GOODA   (1) ----------DHLAPLQLLIFGTAHSLTAIIVQNTDLVDWSFLPHSTIKTFTLYLDQMAT
           TRANSLATION OF ORF111-10   (1) ----YKKAGSDHLAPLQLLIFGTAHSLTAIIVQNTDLVDWSFLPHSTIKTFTLYLDQMAT
                             PGD-P1  (17) ------------------------------------------------------------
                             PGD-P2   (1) ------------------------------------------------------------
                             PGDP3    (1) ------------------------------------------------------------
                          CONSENSUS  (241)           D LAPLQLLIFATAHS TGIIIQNTDLVEWSFLPHSTVKTFTLYLDQMAT

                                          301                                                                  360
GI_4185939_EMB_CAA76879.1_          (298) LIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIF
GI_4185943_EMB_CAA76882.1_          (301) LIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFVGIIDNHYPKTKIF
GI_4185947_EMB_CAA76885.1_          (298) LIGQTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWKIGLANFVGIIDNHYPKTKIF
GI_5931705_EMB_CAB56603.1_          (272) LIGPTRLRIIKLCGNDPDKIVVPLTKEQVRQAFINSGAWQIGLANFVGIIDNHYPKTKIF
                  ENV OF AB047240     (4) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
         TRANSLATION OF P386TOP-LINK  (1) ------------------------------------------------------------
          TRANSLATION OF POL349-LINK  (1) ------------------------------------------------------NHYPKTKIF
                LNCAP-GENOMEA-POLORF  (51) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
TRANSLATION OF LNCAP-POL-GENA-GOODA   (51) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
           TRANSLATION OF ORF111-10   (57) LIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKTKIF
                             PGD-P1  (17) ------------------------------------------------------------
                             PGD-P2   (1) ------------------------------------------------------------
                             PGDP3    (1) ------------------------------------------------------------
                          CONSENSUS  (301) LIGQ RLRII LCGNDPDKI VP  K QVRQAFI SGAW IGLANFLGIIDNHYPKTKIF
```

FIG. 8-3

```
                                        361                                                        420
       GI_4185939_EMB_CAA76879.1_ (358) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
       GI_4185943_EMB_CAA76882.1_ (361) QFLKMTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTQYQSAQRAELVAV
       GI_4185947_EMB_CAA76885.1_ (358) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
       GI_5931705_EMB_CAB56603.1_ (332) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKVAYTGPKERVIKTPYQSAQRAELVAV
                  ENV OF AB047240  (64) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
     TRANSLATION OF P386TOP-LINK    (1) ----------------------------GSSNGKAAYTGPKERVIKTPYQSAQRAELV--
      TRANSLATION OF POL349-LINK   (10) QFLKLTTWILPKITRREP------------------------------------------
           LNCAP-GENOMEA-POLORF   (111) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
TRANSLATION OF LNCAP-POL-GENA-GOODA (111) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
        TRANSLATION OF ORF111-10  (117) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV
                           PGD-P1  (17) ------------------------------------------------------------
                           PGD-P2   (1) ---------------------------------KAAYTGPKERVIKTPC-----------
                            PGDP3   (1) ------------------------------------------------------------
                        CONSENSUS (361) QFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAELVAV

                                        421                                                        480
       GI_4185939_EMB_CAA76879.1_ (418) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
       GI_4185943_EMB_CAA76882.1_ (421) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
       GI_4185947_EMB_CAA76885.1_ (418) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
       GI_5931705_EMB_CAB56603.1_ (392) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSMDDQLNQLFNLLQQTVRKRNFPFYI
                  ENV OF AB047240 (124) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
     TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
      TRANSLATION OF POL349-LINK   (28) ------------------------------------------------------------
           LNCAP-GENOMEA-POLORF   (171) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
TRANSLATION OF LNCAP-POL-GENA-GOODA (171) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
        TRANSLATION OF ORF111-10  (177) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFPFYI
                           PGD-P1  (17) ------------------------------------------------------------
                           PGD-P2  (17) ------------------------------------------------------------
                            PGDP3   (1) ------------------------------------------------------------
                        CONSENSUS (421) ITVLQDFDQPINIISDSAYVVQATRDVETALIKYS DD LNQLFNLLQQTVRKRNFPFYI
```

FIG. 8-4

```
                                          481                                                        540
        GI_4185939_EMB_CAA76879.1_  (478) THIRAHTNLPGPLTKANEQADLLVSSALIKAQELHALTHVNAAGLKNKFDVTWKQAKDIV
        GI_4185943_EMB_CAA76882.1_  (481) THIRAHTNLPGPLTKANEQADLLVSSALIKAQELHALTHVNVAGLKNKFDVTWKQAKDIV
        GI_4185947_EMB_CAA76885.1_  (478) THIRAHTNLPGPLTKANEQADLLVSSALIKAQELHALAHVNAAGLKNKFDVTWKQAKDIV
        GI_5931705_EMB_CAB56603.1_  (452) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELHALTHVNAAGLKNKFDVTWKQAKDIV
                  ENV OF AB047240   (184) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
       TRANSLATION OF P386TOP-LINK  (31)  ------------------------------------------------------------
        TRANSLATION OF POL349-LINK  (28)  ------------------------------------------------------------
             LNCAP-GENOMEA-POLORF   (231) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
TRANSLATION OF LNCAP-POL-GENA-GOODA (231) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
          TRANSLATION OF ORF111-10  (237) THIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAKDIV
                            PGD-P1  (17)  ------------------------------------------------------------
                            PGD-P2  (17)  ------------------------------------------------------------
                             PGDP3  (1)   ------------------------------------------------------------
                         CONSENSUS  (481) THIRAHTNLPGPLTKANEQADLLVSSA IKAQEL ALTHVNAAGLKNKFDVTWKQAKDIV

                                          541                                                        600
        GI_4185939_EMB_CAA76879.1_  (538) QHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC
        GI_4185943_EMB_CAA76882.1_  (541) QHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVSSFGRLSYIHVTVDTYSHFIWATC
        GI_4185947_EMB_CAA76885.1_  (538) QHCTQCQVLHLPTQEAGVNPRGLCPNALWQMDVTHVPSFGRLSYVHVTVDTYSHFIWATC
        GI_5931705_EMB_CAB56603.1_  (512) QHCTQCQVLDLPTQEAGVNPEVCVLMHYGKWMSHMYLHLGRLSYVHVTVDTYSHFMCATC
                  ENV OF AB047240   (244) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
       TRANSLATION OF P386TOP-LINK  (31)  ------------------------------------------------------------
        TRANSLATION OF POL349-LINK  (28)  ------------------------------------------------------------
             LNCAP-GENOMEA-POLORF   (291) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
TRANSLATION OF LNCAP-POL-GENA-GOODA (291) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
          TRANSLATION OF ORF111-10  (297) QHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIWATC
                            PGD-P1  (17)  ------------------------------------------------------------
                            PGD-P2  (17)  ------------------------------------------------------------
                             PGDP3  (1)   ------------------------------------------------------------
                         CONSENSUS  (541) QHCTQCQVLHL TQEAGVNPRGLCPNALWQMD THV SFGRLSYVHVTVDTYSHFIWATC
```

FIG. 8-5

```
                                            601                                                        660
       GI_4185939_EMB_CAA76879.1_   (598) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
       GI_4185943_EMB_CAA76882.1_   (601) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
       GI_4185947_EMB_CAA76885.1_   (598) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
       GI_5931705_EMB_CAB56603.1_   (572) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
                  ENV OF AB047240   (304) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
      TRANSLATION OF P386TOP-LINK    (31) ------------------------------------------------------------
       TRANSLATION OF POL349-LINK    (28) ------------------------------------------------------------
             LNCAP-GENOMEA-POLORF   (351) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
TRANSLATION OF LNCAP-POL-GENA-GOODA (351) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
         TRANSLATION OF ORF111-10   (357) QTGESTSHAKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG
                           PGD-P1    (17) ------------------------------------------------------------
                           PGD-P2    (17) ------------------------------------------------------------
                            PGDP3     (1) ------------------------------------------------------------
                        CONSENSUS   (601) QTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYNSQG

                                            661                                                        720
       GI_4185939_EMB_CAA76879.1_   (658) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT
       GI_4185943_EMB_CAA76882.1_   (661) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT
       GI_4185947_EMB_CAA76885.1_   (658) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAEQHLT
       GI_5931705_EMB_CAB56603.1_   (632) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAE-HLT
                  ENV OF AB047240   (364) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
      TRANSLATION OF P386TOP-LINK    (31) ------------------------------------------------------------
       TRANSLATION OF POL349-LINK    (28) ------------------------------------------------------------
             LNCAP-GENOMEA-POLORF   (411) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
TRANSLATION OF LNCAP-POL-GENA-GOODA (411) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
         TRANSLATION OF ORF111-10   (417) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQHLT
                           PGD-P1    (17) ------------------------------------------------------------
                           PGD-P2    (17) ------------------------------------------------------------
                            PGDP3     (1) ---------------------------------------------------------HLT
                        CONSENSUS   (661) QAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSA QHLT
```

FIG. 8-6

```
                                        721                                                                 780
GI_4185939_EMB_CAA76879.1_    (718) GKKNSPHEGKLIWWKDSKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
GI_4185943_EMB_CAA76882.1_    (721) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
GI_4185947_EMB_CAA76885.1_    (718) GKKNSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
GI_5931705_EMB_CAB56603.1_    (691) GKKNSPHEGKLI------------------------------------------------
                ENV OF AB047240 (424) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
        TRANSLATION OF P386TOP-LINK (31) ------------------------------------------------------------
         TRANSLATION OF POL349-LINK (28) ------------------------------------------------------------
               LNCAP-GENOMEA-POLORF (471) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
TRANSLATION OF LNCAP-POL-GENA-GOODA (471) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
          TRANSLATION OF ORF111-10 (477) GKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI
                           PGD-P1  (17) ------------------------------------------------------------
                           PGD-P2  (17) ------------------------------------------------------------
                            PGDP3   (4) GKKNSPHEGKLIC-------------------------------------------------
                        CONSENSUS  (721) GKK SPHEGKLIWWKD KNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYNEPI

                                        781                                                                 840
GI_4185939_EMB_CAA76879.1_    (778) RDAKKSTSAETETS--------------------------------------------------
GI_4185943_EMB_CAA76882.1_    (781) GDAKKSTSAETETP--------------------------------------------------
GI_4185947_EMB_CAA76885.1_    (778) RDAKKSTSAETETS--------------------------------------------------
GI_5931705_EMB_CAB56603.1_    (703) ------------------------------------------------------------------
                ENV OF AB047240 (484) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
        TRANSLATION OF P386TOP-LINK (31) ------------------------------------------------------------
         TRANSLATION OF POL349-LINK (28) ------------------------------------------------------------
               LNCAP-GENOMEA-POLORF (531) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
TRANSLATION OF LNCAP-POL-GENA-GOODA (531) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
          TRANSLATION OF ORF111-10 (537) GDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVYRYP
                           PGD-P1  (17) ------------------------------------------------------------
                           PGD-P2  (17) ------------------------------------------------------------
                            PGDP3  (17) ------------------------------------------------------------
                        CONSENSUS  (781)  DAKK  S E  T
```

FIG. 8-7

```
                                          841                                                                  900
GI_4185939_EMB_CAA76879.1_   (792) ------------------------------------------------------------
GI_4185943_EMB_CAA76882.1_   (795) ------------------------------------------------------------
GI_4185947_EMB_CAA76885.1_   (792) ------------------------------------------------------------
GI_5931705_EMB_CAB56603.1_   (703) ------------------------------------------------------------
ENV OF AB047240              (544) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF POL349-LINK    (28) ------------------------------------------------------------
LNCAP-GENOMEA-POLORF         (591) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF LNCAP-POL-GENA-GOODA (591) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
TRANSLATION OF ORF111-10     (597) PICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSLKFR
PGD-P1                        (17) ------------------------------------------------------------
PGD-P2                        (17) ------------------------------------------------------------
PGDP3                         (17) ------------------------------------------------------------
CONSENSUS                    (841)

                                          901                                                                  960
GI_4185939_EMB_CAA76879.1_   (792) ----------------------------------QSSTVDSQDEQNGDVRRTDEVAIH
GI_4185943_EMB_CAA76882.1_   (795) ----------------------------------QSSTVDSQDEQNGDVRRTDEVAIH
GI_4185947_EMB_CAA76885.1_   (792) ----------------------------------QSSTVDSQDEQNGDVRRTDEVAIH
GI_5931705_EMB_CAB56603.1_   (703) ------------------------------------------------------------
ENV OF AB047240              (604) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
TRANSLATION OF P386TOP-LINK   (31) ------------------------------------------------------------
TRANSLATION OF POL349-LINK    (28) ------------------------------------------------------------
LNCAP-GENOMEA-POLORF         (651) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
TRANSLATION OF LNCAP-POL-GENA-GOODA (651) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
TRANSLATION OF ORF111-10     (657) PKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQTQS
PGD-P1                        (17) ------------------------------------------------------------
PGD-P2                        (17) ------------------------------------------------------------
PGDP3                         (17) ------------------------------------------------------------
CONSENSUS                    (901)                                  TI
```

FIG. 8-8

```
                                          961                                                                 1020
GI_4185939_EMB_CAA76879.1_      (816) QEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS---
GI_4185943_EMB_CAA76882.1_      (819) QESRAADLGTTKEADAVSYKISREHKGDTNPREYAACGLDDCINGGKSPYACRSSCS---
GI_4185947_EMB_CAA76885.1_      (816) QEGRAANLGTTKEADAVSYKISREHKGDTNPREYAACSLDDCINGGKSPYACRSSCS---
GI_5931705_EMB_CAB56603.1_      (703) ------------------------------------------------------------
ENV OF AB047240                 (664) CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPELWR
TRANSLATION OF P386TOP-LINK      (31) ------------------------------------------------------------
TRANSLATION OF POL349-LINK       (28) ------------------------------------------------------------
LNCAP-GENOMEA-POLORF            (711) CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGP-------
TRANSLATION OF LNCAP-POL-GENA-GOODA (711) CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPELWR
TRANSLATION OF ORF111-10        (717) CPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPELWR
PGD-P1                           (17) ------------------------------------------------------------
PGD-P2                           (17) ------------------------------------------------------------
PGDP3                            (17) ------------------------------------------------------------
CONSENSUS                       (961)         A   D       K           P EWG   I         SP S

                                          1021       1035
GI_4185939_EMB_CAA76879.1_      (873) ---------------
GI_4185943_EMB_CAA76882.1_      (876) ---------------
GI_4185947_EMB_CAA76885.1_      (873) ---------------
GI_5931705_EMB_CAB56603.1_      (703) ---------------
ENV OF AB047240                 (724) LWPDTTLEFGLEIKL
TRANSLATION OF P386TOP-LINK      (31) ---------------
TRANSLATION OF POL349-LINK       (28) ---------------
LNCAP-GENOMEA-POLORF            (764) ---------------
TRANSLATION OF LNCAP-POL-GENA-GOODA (771) LWPDTTLEFGLEIKL
TRANSLATION OF ORF111-10        (777) LWPDTTLEFGLEIKL
PGD-P1                           (17) ---------------
PGD-P2                           (17) ---------------
PGDP3                            (17) ---------------
CONSENSUS                       (1021)
```

FIG. 8-9

```
                                        1                                                          60
GI_4185940_EMB_CAA76880.1_      (1)  ------------------------------------------------------------
GI_4185944_EMB_CAA76883.1_      (1)  ------------------------------------------------------------
GI_4185948_EMB_CAA76886.1_      (1)  ------------------------------------------------------------
GI_5931706_EMB_CAB56604.1_      (1)  ------------------------------------------------------------
            ENV OF AB047240     (1)  MATLIGQGRLRIITLCGNDPDKITVPFNKQQVRQAFISSGAWQIGLANFLGIIDNHYPKT
TRANSLATION OF E207TOP-LINK     (1)  ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1)  ------------------------------------------------------------
  TRANSLATION OF T20.22A-23     (1)  ------------------------------------------------------------
                    PGD-E1      (1)  ------------------------------------------------------------
                    PGD-E2      (1)  ------------------------------------------------------------
                    PGD-E3      (1)  ------------------------------------------------------------
                 CONSENSUS      (1)

                                        61                                                         120
GI_4185940_EMB_CAA76880.1_      (1)  ------------------------------------------------------------
GI_4185944_EMB_CAA76883.1_      (1)  ------------------------------------------------------------
GI_4185948_EMB_CAA76886.1_      (1)  ------------------------------------------------------------
GI_5931706_EMB_CAB56604.1_      (1)  ------------------------------------------------------------
            ENV OF AB047240    (61)  KIFQFLKLTTWILPKITRREPLENALTVFTDGSSNGKAAYTGPKERVIKTPYQSAQRAEL
TRANSLATION OF E207TOP-LINK     (1)  ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1)  ------------------------------------------------------------
  TRANSLATION OF T20.22A-23     (1)  ------------------------------------------------------------
                    PGD-E1      (1)  ------------------------------------------------------------
                    PGD-E2      (1)  ------------------------------------------------------------
                    PGD-E3      (1)  ------------------------------------------------------------
                 CONSENSUS     (61)
```

FIG. 9-1

```
                                        121                                                                 180
GI_4185940_EMB_CAA76880.1_      (1) ------------------------------------------------------------------------
GI_4185944_EMB_CAA76883.1_      (1) ------------------------------------------------------------------------
GI_4185948_EMB_CAA76886.1_      (1) ------------------------------------------------------------------------
GI_5931706_EMB_CAB56604.1_      (1) ------------------------------------------------------------------------
             ENV OF AB047240  (121) VAVITVLQDFDQPINIISDSAYVVQATRDVETALIKYSTDDHLNQLFNLLQQTVRKRNFP
TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------------------
  TRANSLATION OF T20.22A-23     (1) ------------------------------------------------------------------------
                    PGD-E1      (1) ------------------------------------------------------------------------
                    PGD-E2      (1) ------------------------------------------------------------------------
                    PGD-E3      (1) ------------------------------------------------------------------------
                 CONSENSUS    (121)

                                        181                                                                 240
GI_4185940_EMB_CAA76880.1_      (1) ------------------------------------------------------------------------
GI_4185944_EMB_CAA76883.1_      (1) ------------------------------------------------------------------------
GI_4185948_EMB_CAA76886.1_      (1) ------------------------------------------------------------------------
GI_5931706_EMB_CAB56604.1_      (1) ------------------------------------------------------------------------
             ENV OF AB047240  (181) FYITHIRAHTNLPGPLTKANEQADLLVSSAFIKAQELLALTHVNAAGLKNKFDVTWKQAK
TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------------------
  TRANSLATION OF T20.22A-23     (1) ------------------------------------------------------------------------
                    PGD-E1      (1) ------------------------------------------------------------------------
                    PGD-E2      (1) ------------------------------------------------------------------------
                    PGD-E3      (1) ------------------------------------------------------------------------
                 CONSENSUS    (181)
```

FIG. 9-2

```
                                        241                                                                  300
GI_4185940_EMB_CAA76880.1_      (1) ------------------------------------------------------------------------
GI_4185944_EMB_CAA76883.1_      (1) ------------------------------------------------------------------------
GI_4185948_EMB_CAA76886.1_      (1) ------------------------------------------------------------------------
GI_5931706_EMB_CAB56604.1_      (1) ------------------------------------------------------------------------
             ENV OF AB047240  (241) DIVQHCTQCQVLHLSTQEAGVNPRGLCPNALWQMDGTHVPSFGRLSYVHVTVDTYSHFIW
TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------------------
  TRANSLATION OF T20.22A-23     (1) ------------------------------------------------------------------------
                    PGD-E1      (1) ------------------------------------------------------------------------
                    PGD-E2      (1) ------------------------------------------------------------------------
                    PGD-E3      (1) ------------------------------------------------------------------------
                 CONSENSUS    (241)

                                        301                                                                  360
GI_4185940_EMB_CAA76880.1_      (1) ------------------------------------------------------------------------
GI_4185944_EMB_CAA76883.1_      (1) ------------------------------------------------------------------------
GI_4185948_EMB_CAA76886.1_      (1) ------------------------------------------------------------------------
GI_5931706_EMB_CAB56604.1_      (1) ------------------------------------------------------------------------
             ENV OF AB047240  (301) ATCQTGESTSHVKKHLLSCFAVMGVPEKIKTDNGPGYCSKAFQKFLSQWKISHTTGIPYN
TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------------------
  TRANSLATION OF T20.22A-23     (1) ------------------------------------------------------------------------
                    PGD-E1      (1) ------------------------------------------------------------------------
                    PGD-E2      (1) ------------------------------------------------------------------------
                    PGD-E3      (1) ------------------------------------------------------------------------
                 CONSENSUS    (301)
```

FIG. 9-3

```
                                      361                                                                  420
GI_4185940_EMB_CAA76880.1_     (1) -------------------------MQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
GI_4185944_EMB_CAA76883.1_     (1) -------------------------MQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
GI_4185948_EMB_CAA76886.1_     (1) -------------------------MQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
GI_5931706_EMB_CAB56604.1_     (1) ------------------------------------------------------------
            ENV OF AB047240  (361) SQGQAIVERTNRTLKTQLVKQKEGGDSKECTTPQMQLNLALYTLNFLNIYRNQTTTSAKQ
TRANSLATION OF E207TOP-LINK    (1) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (1) ---------------------MNPSEMQRKAPPRRRRHRNRAPLTHKMNKMVTSEEQMKL
                      PGD-E1   (1) ------------------------------------------------------------
                      PGD-E2   (1) ------------------------------------------------------------
                      PGD-E3   (1) ------------------------------------------------------------
                   CONSENSUS  (361)

                                      421                                                                  480
GI_4185940_EMB_CAA76880.1_     (35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
GI_4185944_EMB_CAA76883.1_     (35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
GI_4185948_EMB_CAA76886.1_     (35) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
GI_5931706_EMB_CAB56604.1_     (1) ------------------------------------------------------------
            ENV OF AB047240  (421) HLTGKKHSPHEGKLIWWKDNKNKTWEIGKVITWGRGFACVSPGENQLPVWIPTRHLKFYN
TRANSLATION OF E207TOP-LINK    (1) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (1) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (40) PSTKKAEPPTWAQLKKLTQLATKYLENTKVTQTPESMLLAALMIVSMVVSLPMPAGAAAA
                      PGD-E1   (1) ------------------------------------------------------------
                      PGD-E2   (1) ------------------------------------------------------------
                      PGD-E3   (1) ------------------------------------------------------------
                   CONSENSUS  (421)
```

FIG. 9-4

```
                                      481                                                                 540
GI_4185940_EMB_CAA76880.1_     (95) NYTYWAYVPFPP-LIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY
GI_4185944_EMB_CAA76883.1_     (95) NYTYWAYVPFPP-LIRAVTWMDNPIEVYVNDSVWVPGPTDDHCPAKPEEEGMMINISIGY
GI_4185948_EMB_CAA76886.1_     (95) NYTYWAYVPFPP-LIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY
GI_5931706_EMB_CAB56604.1_      (1) ------------MVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIGY
            ENV OF AB047240    (481) EPIGDAKKRASTEMVTPVTWMDNPIEVYVNDSVWVPGPTDDRCPAKPEEEGMMINISIVY
TRANSLATION OF E207TOP-LINK     (1) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (100) NYTYWAYVPFPP-LIRAVTWMDNPTEVYVNDSVWVPGPIDDRCPAKPEEEGMMINISIGY
                     PGD-E1     (1) ------------------------------------------------------------
                     PGD-E2     (1) ------------------------------------------------------------
                     PGD-E3     (1) ------------------------------------------------------------
                  CONSENSUS    (481)           LI  VTWMDNP EVYVNDSVWVPGP DD CPAKPEEEGMMINISI Y

                                      541                                                                 600
GI_4185940_EMB_CAA76880.1_     (154) HYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNYLQDFSYQRSL
GI_4185944_EMB_CAA76883.1_     (154) RYPPICLGRAPGCLMPAVQNWLVEVPTVSPISRFTYHMVSGMSLRPRVNYLQDFSYQRSF
GI_4185948_EMB_CAA76886.1_     (154) HYPPICLGRAPGCIMPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNYLQDFSYQRSL
GI_5931706_EMB_CAB56604.1_      (48) HYPPICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNCLQDFSYQRSL
            ENV OF AB047240    (541) RYPPICLGRAPGCLMPAVQNWLVEVPTVSPNSRFTYHMVSGMSLRPRVNYLQDFSYQRSL
TRANSLATION OF E207TOP-LINK     (1) ----------------------------------------------------FSYQRSL
 TRANSLATION OF ENV287-LINK     (1) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (159) HYPPICLGRAPGCLMPAVQNWLVEVPTVSPICRFTYHMVSGMSLRPRVNYLQDFSYQRSL
                     PGD-E1     (1) ------------------------------------------------------------
                     PGD-E2     (1) ------------------------------------------------------------
                     PGD-E3     (1) ------------------------------------------------------------
                  CONSENSUS    (541)  YPPICLGRAPGCLMPAVQNWLVEVPTVSP  RFTYHMVSGMSLRPRVN LQDFSYQRSL
```

FIG. 9-5

```
                                      601                                                                 660
GI_4185940_EMB_CAA76880.1_    (214) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
GI_4185944_EMB_CAA76883.1_    (214) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
GI_4185948_EMB_CAA76886.1_    (214) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
GI_5931706_EMB_CAB56604.1_    (108) KFRPKGKTCPKEIPKGSKNTEVLVWEECVANSVVILQNNEFGTIIDWAPRGQFYHNCSGQ
            ENV OF AB047240   (601) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
TRANSLATION OF E207TOP-LINK     (8) KFRPKGKPCPKEIPKESKNTEVL----------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ----------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (219) KFRPKGKPCPKEIPKESKNTEVLVWEECVANSAVILQNNEFGTIIDWAPRGQFYHNCSGQ
                      PGD-E1      (1) --RPKGKPCPKEIPKESC--------------------------------------------
                      PGD-E2      (1) ----------------------------------------------------------------
                      PGD-E3      (1) ----------------------------------------------------------------
                   CONSENSUS    (601) KFRPKGKPCPKEIPKESKNTEVLVWEECVANS VILQNNEFGTIIDWAPRGQFYHNCSGQ

                                      661                                                                 720
GI_4185940_EMB_CAA76880.1_    (274) TQSCQSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPE
GI_4185944_EMB_CAA76883.1_    (274) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIISPVSGPEHPE
GI_4185948_EMB_CAA76886.1_    (274) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPE
GI_5931706_EMB_CAB56604.1_    (168) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYLWEWEEKGISTPRPKIISPVSGPEHPE
            ENV OF AB047240   (661) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPEIISPVSGPEHPE
TRANSLATION OF E207TOP-LINK    (31) ----------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (1) ----------SDLTESLDKHKHKKLQSFYPWEWGEKGI------------------
  TRANSLATION OF T20.22A-23    (279) TQSCPSAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRPKIVSPVSGPEHPE
                      PGD-E1     (17) ----------------------------------------------------------------
                      PGD-E2      (1) ----------------------------------------------------------------
                      PGD-E3      (1) ----------------------------------------------------------------
                   CONSENSUS    (661) TQSC SAQVSPAVDSDLTESLDKHKHKKLQSFYPWEWGEKGISTPRP IISPVSGPEHPE
```

FIG. 9-6

```
                                  721                                                                780
GI_4185940_EMB_CAA76880.1_   (334) LWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGNIVIKP
GI_4185944_EMB_CAA76883.1_   (334) LWRLTVASHHIRIWSGNQTLETRDRKPFYTVDLNSSVTVPLQSCIKPPYMLVVGNIVIKP
GI_4185948_EMB_CAA76886.1_   (334) LWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGNIVIKP
GI_5931706_EMB_CAB56604.1_   (228) LWRLTVASHHIRIWSGNQTLETRYRKPFYTIDLNSILTVPLQSCVKPPYMLVVGNIVIKP
            ENV OF AB047240  (721) LW---------RI----------------------W----------------------P---
TRANSLATION OF E207TOP-LINK  (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK  (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23  (339) LWRLTVASHHIRIWSGNQTLETRDRKPFYTIDLNSSLTVPLQSCVKPPYMLVVGNIVIKP
                     PGD-E1  (17) ------------------------------------------------------------
                     PGD-E2   (1) ------------------------------LNSSLTVPLQSCVKPC------------
                     PGD-E3   (1) ------------------------------------------------------------
                  CONSENSUS  (721) LW         RI                   LNS LTVPLQSCVKP

                                  781                                                                840
GI_4185940_EMB_CAA76880.1_   (394) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKG
GI_4185944_EMB_CAA76883.1_   (394) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWETSPSIHTLTEVLKG
GI_4185948_EMB_CAA76886.1_   (394) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKG
GI_5931706_EMB_CAB56604.1_   (288) ASQTITCENCRLFTCIDSTFNWQHRILLVRAREGMWIPVSTDRPWEASPSIHILTEILKG
            ENV OF AB047240  (727) ----------------DITLEFGLEIKL------------------------------
TRANSLATION OF E207TOP-LINK  (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK  (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23  (399) DSQTITCENCRLLTCIDSTFNWQHRILLVRAREGVWIPVSMDRPWEASPSVHILTEVLKG
                     PGD-E1  (17) ------------------------------------------------------------
                     PGD-E2  (17) ------------------------------------------------------------
                     PGD-E3   (1) ------------------------------------------------------------
                  CONSENSUS  (781)                DST  W   I L
```

FIG. 9-7

```
                                      841                                                        900
GI_4185940_EMB_CAA76880.1_     (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
GI_4185944_EMB_CAA76883.1_     (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
GI_4185948_EMB_CAA76886.1_     (454) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
GI_5931706_EMB_CAB56604.1_     (348) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNYWQKNSTRLWNSQSSI
            ENV OF AB047240    (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK     (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (459) VLNRSKRFIFTLIAVIMGLIAVTATAAVAGVALHSSVQSVNFVNDWQKNSTRLWNSQSSI
                     PGD-E1     (17) ------------------------------------------------------------
                     PGD-E2     (17) ------------------------------------------------------------
                     PGD-E3      (1) ------------------------------------------------------------
                  CONSENSUS    (841)

                                      901                                                        960
GI_4185940_EMB_CAA76880.1_     (514) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH
GI_4185944_EMB_CAA76883.1_     (514) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFSITPQIYNESEHHWDMVRRH
GI_4185948_EMB_CAA76886.1_     (514) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESELHWDMVRRH
GI_5931706_EMB_CAB56604.1_     (408) DQKLASQINDLRQTVIWMGDRLMTLEHHFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH
            ENV OF AB047240    (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK     (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK     (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (519) DQKLANQINDLRQTVIWMGDRLMSLEHRFQLQCDWNTSDFCITPQIYNESEHHWDMVRRH
                     PGD-E1     (17) ------------------------------------------------------------
                     PGD-E2     (17) ------------------------------------------------------------
                     PGD-E3      (1) ------------------------------------------------------------
                  CONSENSUS    (901)
```

FIG. 9-8

```
                                        961                                                                1020
GI_4185940_EMB_CAA76880.1_    (574) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
GI_4185944_EMB_CAA76883.1_    (574) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
GI_4185948_EMB_CAA76886.1_    (574) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
GI_5931706_EMB_CAB56604.1_    (468) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWIKTIRSTMI
            ENV OF AB047240   (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK    (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (579) LQGREDNLTLDISKLKEQIFEASKAHLNLVPGTEAIAGVADGLANLNPVTWVKTIGSTTI
                     PGD-E1     (17) ------------------------------------------------------------
                     PGD-E2     (17) ------------------------------------------------------------
                     PGD-E3      (1) ------------------------------------------------------------
                  CONSENSUS    (961)

                                        1021                                                               1081
GI_4185940_EMB_CAA76880.1_    (634) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
GI_4185944_EMB_CAA76883.1_    (634) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
GI_4185948_EMB_CAA76886.1_    (634) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
GI_5931706_EMB_CAB56604.1_    (528) INLILIVVCLFCLLLVCRCTQQLRRDSDIENGP--------------------------
            ENV OF AB047240   (739) ------------------------------------------------------------
TRANSLATION OF E207TOP-LINK    (31) ------------------------------------------------------------
 TRANSLATION OF ENV287-LINK    (29) ------------------------------------------------------------
  TRANSLATION OF T20.22A-23    (639) INLILILVCLFCLLLVCRCTQQLRRDSDHRERAMMTMAVLSKRKGGNVGKSKRDQIVTVSV
                     PGD-E1     (17) ------------------------------------------------------------
                     PGD-E2     (17) ------------------------------------------------------------
                     PGD-E3      (1) ----------------RCTQQLRRDSDHRERA--------------------------
                  CONSENSUS    (1021)                 RCTQQLRRDSD
```

FIG. 9-9